

SEQUENCE LISTING

<110> ASAHI KASEI KABUSHIKI KAISHA

<120> NF- $\kappa$ B Activating Gene

<130> F101131-US

<150> JP 2000-402288

<151> 2000-12-28

<150> JP 2001-088912

<151> 2001-03-26

<150> JP 2001-254018

<151> 2001-08-24

<150> US 60/258, 315

<151> 2000-12-28

<150> US 60/278, 640

<151> 2001-03-26

<150> US 60/314, 385

<151> 2001-08-24

<160> 182

<170> PatentIn Ver. 2.0

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DATE 02-04-2009 BY 60322 UCBAW/BJS

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20                      25                      30

35                      40                      45

50                      55                      60

65                      70                      75                      80

85                      90                      95

100                      105                      110

2/735





Met Ser Gly Leu Ile Thr Ile Val Val Leu Leu Gly

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Ile Ala Phe Val Val Tyr Lys Leu Phe Leu Ser Asp Gly Gln Tyr Ser

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cct cca ccg tac tct gag tat cct cca ttt tcc cac cgt tac cag aga 325

Pro Pro Pro Tyr Ser Glu Tyr Pro Pro Phe Ser His Arg Tyr Gln Arg

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Phe Thr Asn Ser Ala Gly Pro Pro Pro Pro Gly Phe Lys Ser Glu Phe

45 50 55 60

aca gga cca cag aat act ggc cat ggt gca act tct ggt ttt ggc agt 421

Thr Gly Pro Gln Asn Thr Gly His Gly Ala Thr Ser Gly Phe Gly Ser

65 70 75

gct ttt aca gga caa caa gga tat gaa aat tca gga cca ggg ttc tgg 469

Ala Phe Thr Gly Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp

80 85 90

aca ggc ttg gga act ggt gga ata cta gga tat ttg ttt ggc agc aat 517

Thr Gly Leu Gly Thr Gly Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn

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aga gcg gca aca ccc ttc tca gac tcg tgg tac tac ccg tcc tat cct 565

Arg Ala Ala Thr Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro

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Pro Ser Tyr Pro Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly  
125 130 135 140

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Gly Ser Gly Ser Tyr Ser Val Cys Ser Asn Ser Asp Thr Lys Thr Arg  
145 150 155

act gca tca gga tat ggt ggt acc agg aga cga taaagtagaa agttggagtc 714  
Thr Ala Ser Gly Tyr Gly Gly Thr Arg Arg Arg  
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&lt;210&gt; 3

&lt;211&gt; 339

&lt;212&gt; PRT

⟨213⟩ Homo sapiens

 $\langle 400 \rangle$  3

Met Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu

1                      5                      10                      15

Gly Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn

20 25 30

Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His

35                      40                      45

Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu

50                          55                          60



210 215 220

Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His  
 225 230 235 240

Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr  
 245 250 255

Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile  
 260 265 270

Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp  
 275 280 285

Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn  
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Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys  
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Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr  
 325 330 335

Arg Arg Arg

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<211> 1924

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DATE 04-08-2001 BY 60322 UCBAW



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213

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30

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Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val Ile

70

75

80

cag tgt cag aac aaa ggc tgg gat ggg tat gat gta cag tgg gaa tgt 405

Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu Cys

85

90

95

aag acg gac tta gat att gca tac aaa ttt gga aaa act gtg gtg agc 453

Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val Ser

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105

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tgt gaa ggc tat gag tcc tct gaa gac cag tat gta cta aga ggt tct 501

Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly Ser

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125

tgt ggc ttg gag tat aat tta gat tat aca gaa ctt ggc ctg cag aaa 549

Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln Lys

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ctg aag gag tct gga aag cag cac ggc ttt gcc tct ttc tct gat tat 597

Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp Tyr

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155

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tat tat aag tgg tcc tcg gcg gat tcc tgt aac atg agt gga ttg att 645

Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile

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acc atc gtg gta ctc ctt ggg atc gcc ttt gta gtc tat aag ctg ttc 693

Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe

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ctg agt gac ggg cag tat tct cct cca ccg tac tct gag tat cct cca 741

Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro

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Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro

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cca ggc ttt aag tct gag ttc aca gga cca cag aat act ggc cat ggt 837

Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His Gly

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gca act tct ggt ttt ggc agt gct ttt aca gga caa caa gga tat gaa 885

Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr Glu

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250

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aat tca gga cca ggg ttc tgg aca ggc ttg gga act ggt gga ata cta 933

Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile Leu

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gga tat ttg ttt ggc agc aat aga gcg gca aca ccc ttc tca gac tcg 981

Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser

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tgg tac tac ccg tcc tat cct ccc tcc tac cct ggc acg tgg aat agg 1029

Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn Arg

290 295 300 305

gct tac tca ccc ctt cat gga ggc tcg ggc agc tat tcg gta tgt tca 1077

Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys Ser

310 315 320

aac tca gac acg aaa acc aga act gca tca gga tat ggt ggt acc agg 1125

Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr Arg

325 330 335

aga cga taaagtagaa agttggagtc aaacactgga tgcagaaatt ttggattttt 1181

Arg Arg

catcactttc tcttttagaaa aaaagtacta cctgttaaca attgggaaaa ggggatattc 1241

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atttgggtatt atattatttg atgtttgctg ttcttcaaac atttaaataca agctttggac 1601

taattatgct aatttgtgag ttctgatcac ttttgagctc tgaagctttg aatcattcag 1661



Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala

65 70 75 80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile

85 90 95

Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe

100 105 110

Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Ser

115 120 125

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cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180



Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe Ile Leu Gln Leu

105

110

115

gac att gcc ttc aag cta aac aac caa atc agt taagtgtact ctcctctcat 625

Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Ser

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gtaaaaatgg taatagt

702

<210> 7

<211> 233

<212> PRT

<213> Homo sapiens

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Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile

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Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly

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25

30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val

35

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45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val

ALL INFORMATION CONTAINED HEREIN IS UNCLASSIFIED

50 55 60

Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala  
65 70 75 80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile  
85 90 95

Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe  
100 105 110

Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Arg Glu  
115 120 125

Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala  
130 135 140

Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu  
145 150 155 160

Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr  
165 170 175

Tyr Glu Cys Asp Val Leu Pro Tyr Ala Gln His Leu His His Tyr Gly  
180 185 190

Val Val Leu Glu Glu Asp His His Asp Val Pro Thr Pro Ser Ala Ser  
195 200 205

Gly Lys Ser His Leu Cys Pro Trp Asp Phe His Asp Leu Tyr Gln Tyr

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Pro Ser Gly Met Val Phe His Arg Val

225 230

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cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcacct 180

aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236

Met Ala Gly Ala

1

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284

Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile











1 5 10 15

Leu Ser Cys Leu Ala Leu Ser Val Leu Leu Leu Ala Gln Leu Ser Asp  
20 25 30

Ala Ala Lys Asn Phe Glu Asp Val Arg Cys Lys Cys Ile Cys Pro Pro  
35 40 45

Tyr Lys Glu Asn Ser Gly His Ile Tyr Asn Lys Asn Ile Ser Gln Lys  
50 55 60

Asp Cys Asp Cys Leu His Val Val Glu Pro Met Pro Val Arg Gly Pro  
65 70 75 80

Asp Val Glu Ala Tyr Cys Leu Arg Cys Glu Cys Lys Tyr Glu Glu Arg  
85 90 95

Ser Ser Val Thr Ile Lys Val Thr Ile Ile Ile Tyr Leu Ser Ile Leu  
100 105 110

Gly Leu Leu Leu Leu Tyr Met Val Tyr Leu Thr Leu Val Glu Pro Ile  
115 120 125

Leu Lys Arg Arg Leu Phe Gly His Ala Gln Leu Ile Gln Ser Asp Asp  
130 135 140

Asp Ile Gly Asp His Gln Pro Phe Ala Asn Ala His Asp Val Leu Ala  
145 150 155 160

Arg Ser Arg Ser Arg Ala Asn Val Leu Asn Lys Val Glu Tyr Ala Gln  
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Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Ser Val Phe Asp  
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Arg His Val Val Leu Ser  
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Met Ala Thr Leu Trp Gly Gly Leu Leu

1

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cgg ctt ggc tcc ttg ctc agc ctg tcg tgc ctg gcg ctt tcc gtg ctg 160

Arg Leu Gly Ser Leu Leu Ser Leu Ser Cys Leu Ala Leu Ser Val Leu

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ctg ctg gcg cag ctg tca gac gcc gcc aag aat ttc gag gat gtc aga 208

Leu Leu Ala Gln Leu Ser Asp Ala Ala Lys Asn Phe Glu Asp Val Arg

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tgt aaa tgt atc tgc cct ccc tat aaa gaa aat tct ggg cat att tat 256

Cys Lys Cys Ile Cys Pro Pro Tyr Lys Glu Asn Ser Gly His Ile Tyr

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55

aat aag aac ata tct cag aaa gat tgt gat tgc ctt cat gtt gtg gag 304

Asn Lys Asn Ile Ser Gln Lys Asp Cys Asp Cys Leu His Val Val Glu

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65

70

ccc atg cct gtg cgg ggg cct gat gta gaa gca tac tgt cta cgc tgt 352

Pro Met Pro Val Arg Gly Pro Asp Val Glu Ala Tyr Cys Leu Arg Cys

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gaa tgc aaa tat gaa gaa aga agc tct gtc aca atc aag gtt acc att 400

Glu Cys Lys Tyr Glu Glu Arg Ser Ser Val Thr Ile Lys Val Thr Ile

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105

ata att tat ctc tcc att ttg ggc ctt cta ctt ctg tac atg gta tat 448

Ile Ile Tyr Leu Ser Ile Leu Gly Leu Leu Leu Leu Tyr Met Val Tyr

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115

120

ctt act ctg gtt gag ccc ata ctg aag agg cgc ctc ttt gga cat gca 496

Leu Thr Leu Val Glu Pro Ile Leu Lys Arg Arg Leu Phe Gly His Ala

125

130

135





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&lt;210&gt; 11

 $\langle 211 \rangle$  221

&lt;212&gt; PRT

⟨213⟩ Homo sapiens

&lt;400&gt; 11

Met Ala Leu Ala Leu Ala Ala Leu Ala Ala Val Glu Pro Ala Cys Gly

1

5

10

15

Ser Arg Tyr Gln Gln Leu Gln Asn Glu Glu Glu Ser Gly Glu Pro Glu

20

25

30

Gln Ala Ala Gly Asp Ala Pro Pro Pro Tyr Ser Ser Ile Ser Ala Glu

35

40

45

Ser Ala Ala Tyr Phe Asp Tyr Lys Asp Glu Ser Gly Phe Pro Lys Pro

50

55

60

Pro Ser Tyr Asn Val Ala Thr Thr Leu Pro Ser Tyr Asp Glu Ala Glu

65

70

75

80

Arg Thr Lys Ala Glu Ala Thr Ile Pro Leu Val Pro Gly Arg Asp Glu

85

90

95

Asp Phe Val Gly Arg Asp Asp Phe Asp Asp Ala Asp Gln Leu Arg Ile

100

105

110

Gly Asn Asp Gly Ile Phe Met Leu Thr Phe Phe Met Ala Phe Leu Phe

115

120

125

Asn Trp Ile Gly Phe Phe Leu Ser Phe Cys Leu Thr Thr Ser Ala Ala

130

135

140

Gly Arg Tyr Gly Ala Ile Ser Gly Phe Gly Leu Ser Leu Ile Lys Trp

145

150

155

160

Ile Leu Ile Val Arg Phe Ser Thr Tyr Phe Pro Gly Tyr Phe Asp Gly

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175

Gln Tyr Trp Leu Trp Trp Val Phe Leu Val Leu Gly Phe Leu Leu Phe

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Phe Ser Asn Leu Pro Arg Thr Arg Val Leu Phe Ile Tyr  
210 215 220

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gctcgctctg cttccctgct gccggtgcg cc atg gcg ttg gcg ttg gcg gcg 173  
Met Ala Leu Ala Leu Ala Ala  
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ctg gcg gcg gtc gag ccg gcc tgc ggc agc cgg tac cag cag ttg cag 221  
Leu Ala Ala Val Glu Pro Ala Cys Gly Ser Arg Tyr Gln Gln Leu Gln  
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Asn Glu Glu Glu Ser Gly Glu Pro Glu Gln Ala Ala Gly Asp Ala Pro

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cca cct tac agc agc att tct gca gag agc gca gca tat ttt gac tac 317

Pro Pro Tyr Ser Ser Ile Ser Ala Glu Ser Ala Ala Tyr Phe Asp Tyr

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aag gat gag tct ggg ttt cca aag ccc cca tct tac aat gta gct aca 365

Lys Asp Glu Ser Gly Phe Pro Lys Pro Pro Ser Tyr Asn Val Ala Thr

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aca ctg ccc agt tat gat gaa gcg gag agg acc aag gct gaa gct act 413

Thr Leu Pro Ser Tyr Asp Glu Ala Glu Arg Thr Lys Ala Glu Ala Thr

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Ile Pro Leu Val Pro Gly Arg Asp Glu Asp Phe Val Gly Arg Asp Asp

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Phe Asp Asp Ala Asp Gln Leu Arg Ile Gly Asn Asp Gly Ile Phe Met

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tta act ttt ttc atg gca ttc ctc ttt aac tgg att ggg ttt ttc ctg 557

Leu Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe Leu

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Ser Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile Ser

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Gly Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser

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acc tat ttc cct gga tat ttt gat ggt cag tac tgg ctc tgg tgg gtg 701

Thr Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val

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Phe Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr

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gca aaa gtt cgg aag atg cca gaa act ttc tca aat ctc ccc agg acc 797

Ala Lys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr

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aga gtt ctc ttt att tat taaagatggt ttctggcaaa ggccttctg 845

Arg Val Leu Phe Ile Tyr

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agaaaccagt gggttataat gtagaatgat gtgctttctg cccaagtggg aattcatctt 1805

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[illegible]

&lt;211&gt; 242

&lt;212&gt; PRT

⟨213⟩ Homo sapiens

&lt;400&gt; 13

Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn  
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Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser  
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Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu  
35 40 45

Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val  
50 55 60

Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro  
65 70 75 80

Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu  
85 90 95

Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln  
100 105 110

Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala  
115 120 125

Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe  
130 135 140

Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile  
145 150 155 160

Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu  
165 170 175

Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr  
180 185 190

Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu  
195 200 205

Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg  
210 215 220

Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe  
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Leu Leu

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<211> 2324

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Leu Leu Asn Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro

15 20 25

cct act tca aac cca gca ccg cag att gtg cag gct gcg tct tca gca 147

Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala

30 35 40 45

cca gca ctt gaa act gac tct tcc cct cca cca tat agt agt att act 195

Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr

50 55 60

gtg gaa gta cct aca act tca gat aca gaa gtt tac ggt gag ttt tat 243

Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr

65 70 75

ccc gtg cca cct ccc tat agc gtt gct acc tct ctt cct aca tac gat 291

Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp

80

85

90

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 95 100 105

aca tct caa aga att cag gag gaa gag tgt cca cca aga gat gac ttc 387  
 Thr Ser Gln Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe  
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agt gat gca gac cag ctc aga gtg ggg aat gat ggc att ttc atg ctg 435  
 Ser Asp Ala Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu  
 130 135 140

gca ttt ttc atg gca ttt att ttc aac tgg ctt gga ttt tgt tta tcc 483  
 Ala Phe Phe Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser  
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 160 165 170

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 Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp  
 175 180 185

tat ttt act gga tat ttc aat gga cag tat tgg ctt tgg tgg ata ttt 627  
 Tyr Phe Thr Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe  
 190 195 200 205

ctt gta ctt ggc ctg ctc ctt ttc ttc aga gga ttt gtt aat tat cta 675

Leu Val Leu Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu

210

215

220

aaa gtc aga aac atg tct gaa agt atg gca gct gct cat aga aca agg 723

Lys Val Arg Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg

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tat ttc ttc tta ttg tagagactgc atcaaccgca cattcctttc ttataccaat 778

Tyr Phe Phe Leu Leu

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gcatatagga ctgtggggtc tgtgtgtgta gtgagagtgt gtagccacta ttataactgg 1978

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20 25 30

Asn Pro Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu

35 40 45

Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val

50 55 60

Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro

65 70 75 80

Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu

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95

Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln

100

105

110

Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala

115

120

125

Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe

130

135

140

Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile

145

150

155

160

Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu

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170

175

Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr

180

185

190

Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu

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205

Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg

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Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe

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Leu Leu

<210> 16

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Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val

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ctt ctt aat gaa gag gat aac tca gaa tca tcg gct ata gag cag cca 99

Leu Leu Asn Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro

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25

cct act tca aac cca gca ccg cag att gtg cag gct gtg tct tca gca 147

Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala

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cca gca ctt gaa act gac tct tcc cct cca cca tat agt agt att act 195

Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr

50

55

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gtg gaa gta cct aca act tca gat aca gaa gtt tac ggt gag ttt tat 243  
Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr  
65 70 75

ccc gtg cca cct ccc tat agc gtt gct acc tct ctt cct aca tac gat 291  
Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp  
80 85 90

gaa gct gag aag gct aaa gct gct gca atg gca gct gca gca gca gaa 339  
Glu Ala Glu Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu  
95 100 105

aca tct caa aga att cag gag gaa gag tgt cca cca aga gat gac ttc 387  
Thr Ser Gln Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe  
110 115 120 125

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Ser Asp Ala Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu  
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gca ttt ttc atg gca ttt att ttc aac tgg ctt gga ttt tgt tta tcc 483  
Ala Phe Phe Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser  
145 150 155

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Phe Cys Ile Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly  
160 165 170





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- <212> PRT
- <213> Homo sapiens

<400> 17

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Leu Asn Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr  
20 25 30

Asn Ala Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu  
45/735

35                      40                      45  
 Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro  
 50                      55                      60  
 Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly  
 65                      70                      75                      80  
 Glu Asp Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp  
 85                      90                      95  
 His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu  
 100                      105                      110  
 Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro  
 115                      120                      125  
 Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu Glu Thr  
 130                      135                      140  
 Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr  
 145                      150                      155                      160  
 Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro  
 165                      170                      175  
 Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala  
 180                      185                      190

Lys Ala Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile

195

200

205

Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln

210

215

220

Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala

225

230

235

240

Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn

245

250

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Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu

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265

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Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr

275

280

285

Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu

290

295

300

Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met

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Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn

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agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg 154

Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala

20

25

30

gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg 202

Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro

35

40

45

50

ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg 250

Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro Ala Ala

55

60

65



Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala

180 185 190

gct gca atg gca gct gca gca gca gaa aca tct caa aga att cag gag 682

Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu

195 200 205 210

gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga 730

Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg

215 220 225

gtg ggg aat gat ggc att ttc atg ctg gca ttt ttc atg gca ttt att 778

Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile

230 235 240

ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata 826

Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile

245 250 255

gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa 874

Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys

260 265 270

tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat 922

Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn

275 280 285 290

gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt 970

Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu Leu



295

300

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ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa 1018  
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310 315 320

agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg 1060  
Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu  
325 330 335

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<212> PRT

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<400> 19

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Leu Asn Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr

20 25 30

Asn Ala Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu

35 40 45

Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro

50 55 60

Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly

65 70 75 80

Glu Asp Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp





cttacttttc catctctec caccagcta taccctccca ctggcggcgc gg atg gca 58

Met Ala

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cgc cgg cgg agc cag cga gtc tgc gcg agc ggt ccg agc atg ctc aat 106

Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn

5

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agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg 154

Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala

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gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg 202

Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro

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Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro Ala Ala

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Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His

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cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac 394

Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn

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Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro

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cag att gtg cag gct gcg tct tca gca cca gca ctt gaa act gac tct 490

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Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser

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Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro Tyr Ser

165

170

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gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct 634

Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala

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gct gca atg gca gct gca gca gca gaa aca tct caa aga att cag gag 682

Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu

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200

205

210

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Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile

230

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ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata 826

Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile

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250

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gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa 874

Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys

260

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Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn

275

280

285

290

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Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu Leu

295

300

305

ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa 1018

Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu

310

315

320

agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg 1060

Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu

325

330

335



tagagactgc atcaaccga cattccttcc ttataccaat gtgaaatttc cagatcatct 1120

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<211> 76

<212> PRT

<213> Homo sapiens

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Lys Lys Phe Leu Glu Pro Tyr Ile Tyr Pro Leu Val Ser Pro Phe Val

20

25

30

Ser Arg Ile Trp Pro Lys Lys Ala Ile Gln Glu Ser Asn Asp Thr Asn

35

40

45

Lys Gly Lys Val Asn Phe Lys Gly Ala Asp Met Asn Gly Leu Pro Thr

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Lys Gly Pro Thr Glu Ile Cys Asp Lys Lys Lys Asp

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<210> 22

<211> 1085

<212> DNA

<213> Homo sapiens

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<221> CDS

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cggcctccgc ggtgcctgcc ttcgctctca gggtgaggag ctcaagcttg ggaaa atg 178

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gtg tgc att cct tgt atc gtc att cca gtt ctg ctc tgg atc tac aaa 226

Val Cys Ile Pro Cys Ile Val Ile Pro Val Leu Leu Trp Ile Tyr Lys

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aaa ttc ctg gag cca tat ata tac cct ctg gtt tcc ccc ttc gtt agt 274

Lys Phe Leu Glu Pro Tyr Ile Tyr Pro Leu Val Ser Pro Phe Val Ser

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25

30

cgt ata tgg cct aag aaa gca ata caa gaa tcc aat gat aca aac aaa 322

Arg Ile Trp Pro Lys Lys Ala Ile Gln Glu Ser Asn Asp Thr Asn Lys

35

40

45

ggc aaa gta aac ttt aag ggt gca gac atg aat gga tta cca aca aaa 370

Gly Lys Val Asn Phe Lys Gly Ala Asp Met Asn Gly Leu Pro Thr Lys

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gga cca aca gaa atc tgt gat aaa aag aaa gac taaagaaatt ttcctaaagg 423

Gly Pro Thr Glu Ile Cys Asp Lys Lys Lys Asp

70

75

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tt 1085

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<211> 84

<212> PRT

<213> Homo sapiens

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Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile

35 40 45

Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr Trp

50 55 60

Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His Ser

65 70 75 80

Leu Ser Gly Leu

<210> 24

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<212> DNA

<213> Homo sapiens

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<222> (65)..(316)

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Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile

1

5

10

15

ctg ccg gaa att cag aag cca gag agg aag att cag ttt aag gag aaa 157

Leu Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys

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25

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gtg ctg tgg acc gct atc acc ctc ttt atc ttc tta gtg tgc tgc cag 205

Val Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln

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att ccc ctg ttt ggg atc atg tct tca gat tca gct gac cct ttc tat 253

Ile Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr

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tgg atg aga gtg att cta gcc tct aac aga ggc aca ttg atg gag cac 301

Trp Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His

65

70

75

tct ctc tct ggc ctt tagggagtcc cctcttagga caggcactgc ccagcagcaa 356

Ser Leu Ser Gly Leu

80

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Val Tyr Ile Val Phe Met Leu Gly Ser Cys Ala Phe Phe Ser Lys Thr

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75

80

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Trp Ile Glu Val Ser Gly Ser Ser Ala Lys Asp Val Ala Lys Gln Leu

85

90

95

aag gag cag cag atg gtg atg aga ggc cac cga gag acc tcc atg gtc 452

Lys Glu Gln Gln Met Val Met Arg Gly His Arg Glu Thr Ser Met Val

100

105

110

cat gaa ctc aac cgg tac atc ccc aca gcc gcg gcc ttt ggt ggg ctg 500

His Glu Leu Asn Arg Tyr Ile Pro Thr Ala Ala Ala Phe Gly Gly Leu

115

120

125

tgc atc ggg gcc ctc tcg gtc ctg gct gac ttc cta ggc gcc att ggg 548

Cys Ile Gly Ala Leu Ser Val Leu Ala Asp Phe Leu Gly Ala Ile Gly

130

135

140

145

tct gga acc ggg atc ctg ctc gca gtc aca atc atc tac cag tac ttt 596

Ser Gly Thr Gly Ile Leu Leu Ala Val Thr Ile Ile Tyr Gln Tyr Phe

150

155

160

gag atc ttc gtt aag gag caa agc gag gtt ggc agc atg ggg gcc ctg 644

Glu Ile Phe Val Lys Glu Gln Ser Glu Val Gly Ser Met Gly Ala Leu

165

170

175



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<211> 279

<212> PRT

<213> Homo sapiens

<400> 27

Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp

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Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr

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30

Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg

35

40

45

Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val

50

55

60

Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe

65

70

75

80

Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val

85

90

95

Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp

100

105

110

Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe

115

120

125

Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His

130

135

140

His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro

145

150

155

160

Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val

165

170

175

Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln

180

185

190

Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln

195

200

205

Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser  
 210 215 220

Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly  
 225 230 235 240

Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr  
 245 250 255

Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly  
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Ile Ala Lys Val Lys Ala Asn  
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<210> 28

<211> 1472

<212> DNA

<213> Homo sapiens

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Ser Val Val Thr Ile Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu

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25

30

Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Thr Ser

35

40

45

Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro

50

55

60

Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln

65

70

75

80

Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr

85

90

95

Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly

100

105

110

Gly Ala Ala Ala Pro Tyr Pro Ala Ser Gln Pro Pro Tyr Asn Pro Ala

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120

125

Tyr Met Asp Ala Pro Lys Ala Ala Leu

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<211> 1788

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ctctgggtga aggcagaggc taac atg ggg ttc gga gcg acc ttg gcc gtt 171

Met Gly Phe Gly Ala Thr Leu Ala Val

1

5

ggc ctg acc atc ttt gtg ctg tct gtc gtc act atc atc atc tgc ttc 219



125

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35

40

45

Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro

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55

60

Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln

65

70

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80

Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr

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Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly

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Met Gly Phe Gly Ala Thr Leu Ala

1

5

gtt ggc ctg acc atc ttt gtg ctg tct gtc gtc act atc atc atc tgc 162

Val Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys

10

15

20

ttc acc tgc tcc tgc tgc tgc ctt tac aag acg tgc cgc cga cca cgt 210

Phe Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg

25

30

35

40

ccg gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc cct tat 258

Pro Val Val Thr Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr

45

50

55

cct cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag 306

Pro Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln

60

65

70

ggc tac cac acc atg ccg cct cag cca ggg atg cca gca gca ccc tac 354

Gly Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr

75

80

85

cca atg cag tac cca cca cct tac cca gcc cag ccc atg ggc cca ccg 402

Pro Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro

90

95

100



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<210> 33

<211> 168

<212> PRT

ALL INFORMATION CONTAINED HEREIN IS UNCLASSIFIED  
DATE 01-09-2001 BY 60322 UCBAW

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Pro Pro Gly Asn Pro Val Tyr Pro Gln Thr Leu His Leu Pro Gln Ala  
20 25 30

Pro Pro Tyr Thr Asp Ala Pro Pro Ala Tyr Ser Glu Leu Tyr Arg Pro  
35 40 45

Ser Phe Val His Pro Gly Ala Ala Thr Val Pro Thr Met Ser Ala Ala  
50 55 60

Phe Pro Gly Ala Ser Leu Tyr Leu Pro Met Ala Gln Ser Val Ala Val  
65 70 75 80

Gly Pro Leu Gly Ser Thr Ile Pro Met Ala Tyr Tyr Pro Val Gly Pro  
85 90 95

Ile Tyr Pro Pro Gly Ser Thr Val Leu Val Glu Gly Gly Tyr Asp Ala  
100 105 110

Gly Ala Arg Phe Gly Ala Gly Ala Thr Ala Gly Asn Ile Pro Pro Pro  
115 120 125

Pro Pro Gly Cys Pro Pro Asn Ala Ala Gln Leu Ala Val Met Gln Gly  
130 135 140



Gln Ala Pro Pro Tyr Thr Asp Ala Pro Pro Ala Tyr Ser Glu Leu Tyr  
35 40 45

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50 55 60

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Ala Ala Phe Pro Gly Ala Ser Leu Tyr Leu Pro Met Ala Gln Ser Val  
65 70 75

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Gly Pro Ile Tyr Pro Pro Gly Ser Thr Val Leu Val Glu Gly Gly Tyr  
95 100 105 110

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Asp Ala Gly Ala Arg Phe Gly Ala Gly Ala Thr Ala Gly Asn Ile Pro  
115 120 125

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Pro Pro Pro Pro Gly Cys Pro Pro Asn Ala Ala Gln Leu Ala Val Met  
130 135 140

cag gga gcc aac gtc ctc gta act cag cgg aag ggg aac ttc ttc atg 543  
Gln Gly Ala Asn Val Leu Val Thr Gln Arg Lys Gly Asn Phe Phe Met  
89/735

145

150

155

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Gly Gly Ser Asp Gly Gly Tyr Thr Ile Trp

160

165

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Arg Gly Ile Glu Ile Thr Val Asn Tyr Leu Gly Ile Gln Phe Asp Val  
325 330 335

Lys Phe Trp Ser Gln His Ile Ser Phe Ile Leu Val Gly Ile Ile Ile  
340 345 350

Val Thr Ser Ile Arg Gly Leu Leu Ile Thr Leu Thr Lys Phe Phe Tyr  
355 360 365

Ala Ile Ser Ser Ser Lys Ser Ser Asn Val Ile Val Leu Leu Leu Ala  
370 375 380

Gln Ile Met Gly Met Tyr Phe Val Ser Ser Val Leu Leu Ile Arg Met  
385 390 395 400

Ser Met Pro Leu Glu Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu  
405 410 415

Leu Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val  
420 425 430

Ser Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala  
435 440 445

Pro Glu Lys Gln Met Ala Pro  
450 455





165

170

175

ctc agg aat gtg act gac acg gat att cta gcc ctg gaa cgg cga ctg 694  
Leu Arg Asn Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu

180

185

190

ctg caa acc atg gat atg atc ata agc aaa aag aaa agg atg gca atg 742  
Leu Gln Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala Met

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gca cgg aga aca atg ttc cag aag ggg gaa gtg cat aac aaa cca tca 790  
Ala Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro Ser

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215

220

225

ggt ttc tgg gga atg ata aaa agt gtt acc act tca gca tca gga agt 838  
Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly Ser

230

235

240

gaa aat ctt act ctt att caa cag gaa gtg gat gct ttg gaa gaa tta 886  
Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu Glu Leu

245

250

255

agc agg cag ctt ttt ctg gaa aca gct gat cta tat gct acc aag gag 934  
Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala Thr Lys Glu

260

265

270

aga ata gaa tac tcc aaa acc ttc aag ggg aaa tat ttt aat ttt ctt 982  
Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr Phe Asn Phe Leu

275

280

285





atg cct tta gaa tac cgc acc ata atc act gaa gtc ctt gga gaa ctg 1366

Met Pro Leu Glu Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu Leu

405

410

415

cag ttc aac ttc tat cac cgt tgg ttt gat gtg atc ttc ctg gtc agc 1414

Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val Ser

420

425

430

gct ctc tct agc ata ctc ttc ctc tat ttg gct cac aaa cag gca cca 1462

Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala Pro

435

440

445

gag aag caa atg gca cct tgaacttaag cctactacag actgttagag 1510

Glu Lys Gln Met Ala Pro

450

455

gccagtgggt tcaaaattta gatataagag gggggaaaaa tggaaccagg gcctgacatt 1570

ttataaaca acaaaatgct atggtagcat ttttcacctt catagcatac tccttccccg 1630

tcaggtgata ctatgaccat gagtagcatc agccagaaca tgagagggag aactaactca 1690

agacaatact cagcagagag catcccgtgt ggatatgagg ctggtgtaga ggcggagagg 1750

agccaagaaa ctaaaggtga aaaatacact ggaactctgg ggcaagacat gtctatggta 1810

gctgagccaa acacgtagga tttccgtttt aaggttcaca tggaagaggt tatagctttg 1870

ccttgagatt gactcattaa aatcagagac tgt 1903



Ser Leu Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val Asp  
 115 120 125

Lys Ser Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser Leu  
 130 135 140

Leu Ser Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln Leu  
 145 150 155 160

Thr Leu Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val Val  
 165 170 175

Gln Glu His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro Asp  
 180 185 190

Met Glu Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp Phe  
 195 200 205

Pro Tyr Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met Thr  
 210 215 220

Pro Ala Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly Leu  
 225 230 235 240

Ala Glu Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser Gly  
 245 250 255

Lys Lys Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg Arg  
 260 265 270









tgacggcggc ggaacccaaa gctgccctct ccgtgcaatg tcaactgctcg tgtggtctcc 1317

agcaagggat tcgggcgaag acaaacggat gcacccgtct ttagaaccaa aaatattctc 1377

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gtccctagca t 1448

<210> 39

<211> 313

<212> PRT

<213> Homo sapiens

<400> 39

Met Ala Gly Gln Pro Gly His Met Pro His Gly Gly Ser Ser Asn Asn

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Leu Cys His Thr Leu Gly Pro Val His Pro Pro Asp Pro Gln Arg His

20 25 30

Pro Asn Thr Leu Ser Phe Arg Cys Ser Leu Ala Asp Phe Gln Ile Glu

35 40 45

Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val Tyr Lys Ala Thr Cys

50 55 60

Leu Leu Asp Arg Lys Thr Val Ala Leu Lys Lys Val Gln Ile Phe Glu

65 70 75 80



Met Met Asp Ala Lys Ala Arg Gln Asp Cys Val Lys Glu Ile Gly Leu  
85 90 95

Leu Lys Gln Leu Asn His Pro Asn Ile Ile Lys Tyr Leu Asp Ser Phe  
100 105 110

Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu Leu Ala Asp Ala Gly  
115 120 125

Asp Leu Ser Gln Met Ile Lys Tyr Phe Lys Lys Gln Lys Arg Leu Ile  
130 135 140

Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln Leu Cys Ser Ala Val  
145 150 155 160

Glu His Met His Ser Arg Arg Val Met His Arg Asp Ile Lys Pro Ala  
165 170 175

Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys Leu Gly Asp Leu Gly  
180 185 190

Leu Gly Arg Phe Phe Ser Ser Glu Thr Thr Ala Ala His Ser Leu Val  
195 200 205

Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His Glu Asn Gly Tyr  
210 215 220

Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu Leu Tyr Glu Met  
107/735

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225                      230                      235                      240

Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met Asn Leu Phe Ser

                    245                      250                      255

Leu Cys Gln Lys Ile Glu Gln Cys Asp Tyr Pro Pro Leu Pro Gly Glu

                    260                      265                      270

His Tyr Ser Glu Lys Leu Arg Glu Leu Val Ser Met Cys Ile Cys Pro

                    275                      280                      285

Asp Pro His Gln Arg Pro Asp Ile Gly Tyr Val His Gln Val Ala Lys

                    290                      295                      300

Gln Met His Ile Trp Met Ser Ser Thr

305                      310

<210> 40

<211> 1597

<212> DNA

<213> Homo sapiens

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<400> 40

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ctccagccgc ccgcgggcca gcgcaccggt cccccagcgg cagccgagcc cgccccgcgcg 120

ccgttcgtgc cctcgtgagg ctggcatgca gg atg gca gga cag ccc ggc cac 173

Met Ala Gly Gln Pro Gly His

1

5

atg ccc cat gga ggg agt tcc aac aac ctc tgc cac acc ctg ggg cct 221

Met Pro His Gly Gly Ser Ser Asn Asn Leu Cys His Thr Leu Gly Pro

10

15

20

gtg cat cct cct gac cca cag agg cat ccc aac acg ctg tct ttt cgc 269

Val His Pro Pro Asp Pro Gln Arg His Pro Asn Thr Leu Ser Phe Arg

25

30

35

tgc tcg ctg gcg gac ttc cag atc gaa aag aag ata ggc cga gga cag 317

Cys Ser Leu Ala Asp Phe Gln Ile Glu Lys Lys Ile Gly Arg Gly Gln

40

45

50

55

ttc agc gag gtg tac aag gcc acc tgc ctg ctg gac agg aag aca gtg 365

Phe Ser Glu Val Tyr Lys Ala Thr Cys Leu Leu Asp Arg Lys Thr Val

60

65

70

gct ctg aag aag gtg cag atc ttt gag atg atg gac gcc aag gcg agg 413

Ala Leu Lys Lys Val Gln Ile Phe Glu Met Met Asp Ala Lys Ala Arg

75

80

85

cag gac tgt gtc aag gag atc ggc ctc ttg aag caa ctg aac cac cca 461

Gln Asp Cys Val Lys Glu Ile Gly Leu Leu Lys Gln Leu Asn His Pro



ccg gag agg atc cat gag aac ggc tac aac ttc aag tcc gac atc tgg 845

Pro Glu Arg Ile His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp

220

225

230

tcc ttg ggc tgt ctg ctg tac gag atg gca gcc ctc cag agc ccc ttc 893

Ser Leu Gly Cys Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe

235

240

245

tat gga gat aag atg aat ctc ttc tcc ctg tgc cag aag atc gag cag 941

Tyr Gly Asp Lys Met Asn Leu Phe Ser Leu Cys Gln Lys Ile Glu Gln

250

255

260

tgt gac tac ccc cca ctc ccc ggg gag cac tac tcc gag aag tta cga 989

Cys Asp Tyr Pro Pro Leu Pro Gly Glu His Tyr Ser Glu Lys Leu Arg

265

270

275

gaa ctg gtc agc atg tgc atc tgc cct gac ccc cac cag aga cct gac 1037

Glu Leu Val Ser Met Cys Ile Cys Pro Asp Pro His Gln Arg Pro Asp

280

285

290

295

atc gga tac gtg cac cag gtg gcc aag cag atg cac atc tgg atg tcc 1085

Ile Gly Tyr Val His Gln Val Ala Lys Gln Met His Ile Trp Met Ser

300

305

310

agc acc tgagcgtgga tgcaccgtgc cttatcaaag ccagcaccac tttgccttac 1141

Ser Thr

ttgagtcgtc ttctcttcga gtggccacct ggtagcctag aacagctaag accacagggt 1201

tcagcagggtt ccccaaaagg ctgcccagcc ttacagcaga tgctgaagge agagcagctg 1261

agggaggggc gctggccaca tgtcactgat ggtcagattc caaagtcctt tctttatact 1321

gttgtggaca atctcagctg ggtcaataag ggcagggtgt tcagcgagcc acggcagccc 1381

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tatgctaaca ggagacttgc aggagaccgt gtgatttgtg tagtgagcct ttgaaaatgg 1501

ttagtaccgg gttcagttta gttcttggtg tcttttcaat caagctgtgt gcttaattta 1561

ctctgttgta aagggataaa gtggaaatca tttttt 1597

<210> 41

<211> 371

<212> PRT

<213> Homo sapiens

<400> 41

Met Ser His Glu Lys Ser Phe Leu Val Ser Gly Asp Asn Tyr Pro Pro

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15

Pro Asn Pro Gly Tyr Pro Gly Gly Pro Gln Pro Pro Met Pro Pro Tyr

20

25

30

Ala Gln Pro Pro Tyr Pro Gly Ala Pro Tyr Pro Gln Pro Pro Phe Gln

35

40

45

Pro Ser Pro Tyr Gly Gln Pro Gly Tyr Pro His Gly Pro Ser Pro Tyr  
50 55 60

Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro  
65 70 75 80

Gln Gly Pro Tyr Pro Gln Glu Gly Tyr Pro Gln Gly Pro Tyr Pro Gln  
85 90 95

Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Ser Pro Phe Pro Pro Asn  
100 105 110

Pro Tyr Gly Gln Pro Gln Val Phe Pro Gly Gln Asp Pro Asp Ser Pro  
115 120 125

Gln His Gly Asn Tyr Gln Glu Glu Gly Pro Pro Ser Tyr Tyr Asp Asn  
130 135 140

Gln Asp Phe Pro Ala Thr Asn Trp Asp Asp Lys Ser Ile Arg Gln Ala  
145 150 155 160

Phe Ile Arg Lys Val Phe Leu Val Leu Thr Leu Gln Leu Ser Val Thr  
165 170 175

Leu Ser Thr Val Ser Val Phe Thr Phe Val Ala Glu Val Lys Gly Phe  
180 185 190

Val Arg Glu Asn Val Trp Thr Tyr Tyr Val Ser Tyr Ala Val Phe Phe  
195 200 205

Ile Ser Leu Ile Val Leu Ser Cys Cys Gly Asp Phe Arg Arg Lys His  
210 215 220

Pro Trp Asn Leu Val Ala Leu Ser Val Leu Thr Ala Ser Leu Ser Tyr  
225 230 235 240

Met Val Gly Met Ile Ala Ser Phe Tyr Asn Thr Glu Ala Val Ile Met  
245 250 255

Ala Val Gly Ile Thr Thr Ala Val Cys Phe Thr Val Val Ile Phe Ser  
260 265 270

Met Gln Thr Arg Tyr Asp Phe Thr Ser Cys Met Gly Val Leu Leu Val  
275 280 285

Ser Met Val Val Leu Phe Ile Phe Ala Ile Leu Cys Ile Phe Ile Arg  
290 295 300

Asn Arg Ile Leu Glu Ile Val Tyr Ala Ser Leu Gly Ala Leu Leu Phe  
305 310 315 320

Thr Cys Phe Leu Ala Val Asp Thr Gln Leu Leu Leu Gly Asn Lys Gln  
325 330 335

Leu Ser Leu Ser Pro Glu Glu Tyr Val Phe Ala Ala Leu Asn Leu Tyr  
340 345 350









tgc ttc acc gtc gtc atc ttc tcc atg cag acc cgc tac gac ttc acc 930  
 Cys Phe Thr Val Val Ile Phe Ser Met Gln Thr Arg Tyr Asp Phe Thr  
 265 270 275 280

tca tgc atg ggc gtg ctc ctg gtg agc atg gtg gtg ctc ttc atc ttc 978  
 Ser Cys Met Gly Val Leu Leu Val Ser Met Val Val Leu Phe Ile Phe  
 285 290 295

gcc att ctc tgc atc ttc atc cgg aac cgc atc ctg gag atc gtg tac 1026  
 Ala Ile Leu Cys Ile Phe Ile Arg Asn Arg Ile Leu Glu Ile Val Tyr  
 300 305 310

gcc tca ctg ggc gct ctg ctc ttc acc tgc ttc ctc gca gtg gac acc 1074  
 Ala Ser Leu Gly Ala Leu Leu Phe Thr Cys Phe Leu Ala Val Asp Thr  
 315 320 325

cag ctg ctg ctg ggg aac aag cag ctg tcc ctg agc cca gaa gag tat 1122  
 Gln Leu Leu Leu Gly Asn Lys Gln Leu Ser Leu Ser Pro Glu Glu Tyr  
 330 335 340

gtg ttt gct gcg ctg aac ctg tac aca gac atc atc aac atc ttc ctg 1170  
 Val Phe Ala Ala Leu Asn Leu Tyr Thr Asp Ile Ile Asn Ile Phe Leu  
 345 350 355 360

tac atc ctc acc atc att ggc cgc gcc aag gag tagccgagct ccagctcgct 1223  
 Tyr Ile Leu Thr Ile Ile Gly Arg Ala Lys Glu  
 365 370

gtgcccgcgc aggtggcagc gctggcctgg accctgcccc tggcaccgca gtgccagctg 1283

tacttcccct ctctcttgtc cccaggcaca gcctagggaa aaggatgcct ctctccaacc 1343

ctctgtatg tacactgcag atacttccat ttggaccgcg tgtggccaca gcatggcccc 1403

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tactcattgt tgcattgagc ctgtctgcca gccaccccca gggactgggg gcagcaccag 1523

gtcccgggga gagggattga gccaaagaggt gaggggtgcac gtcttccctc ctgtcccage 1583

tccccagcct ggcgtagagc acccctcccc tccccccac cccctggag tgctgccctc 1643

tggggacatg cggagtgggg gtcttatccc tgtgctgagc cctgagggca gagaggatgg 1703

catgtttcag gggaggggga agccttctc tcaatttggt gtcagtga aa ttccaataaa 1763

tgggatttgc tctctgcc 1781

<210> 43

<211> 393

<212> PRT

<213> Homo sapiens

<400> 43

Met Ser Asp Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala

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Ser Ser Pro Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro

20 25 30

Ala Ala Ser Glu Gly Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu

35 40 45

Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu

50 55 60

Gln Ser Arg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr

65 70 75 80

Leu Arg Leu Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg

85 90 95

Gln Gly Leu Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met

100 105 110

Glu Gly Ala Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg

115 120 125

Lys Ala Gly Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln

130 135 140

Glu Glu Val Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala

145 150 155 160

Met Thr Phe Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala

165

170

175

Tyr Met Val Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val

180

185

190

Leu Val His Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu

195

200

205

Cys Arg Thr Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser

210

215

220

Lys His Glu Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr

225

230

235

240

His Thr Thr Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly

245

250

255

Val Asp Ile Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly

260

265

270

Tyr Asn Leu Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala

275

280

285

Asn Leu Leu Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr

290

295

300

Trp Trp Asn Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn

305

310

315

320





gag aga gag gta gcc gag gca gcg acc ggg gaa gac gcc tct tcg ccg 106

Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala Ser Ser Pro

5

10

15

cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc 154

Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser

20

25

30

35

gaa ggg gcc gcc gcc gcc gcc gcc tgc ccg cca ctg ctg cgc tgc cta 202

Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu

40

45

50

gtg ctc acc ggc ttt gga ggc tac gac aag gtg aag ctg cag agc cgg 250

Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg

55

60

65

ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg 298

Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu

70

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cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg 346

Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu

85

90

95

tac gac cgt ctc ccg cct ctg cct gtc act ccg ggc atg gag ggc gcg 394

Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala

100

105

110

115

ggt gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga 442  
 Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly  
 120 125 130

gac cgg gtg atg gtg ttg aac cgg tca ggg atg tgg cag gaa gag gtg 490  
 Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val  
 135 140 145

act gtg ccc tcg gtc cag acc ttc ctg att cct gag gcc atg acc ttt 538  
 Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe  
 150 155 160

gag gaa gct gct gcc ttg ctc gtc aat tac att aca gcc tac atg gtc 586  
 Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val  
 165 170 175

ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gta cac 634  
 Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His  
 180 185 190 195

atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca 682  
 Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr  
 200 205 210

gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag 730  
 Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu  
 215 220 225

gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act 778  
 124/735

Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr

230

235

240

gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att 826

Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile

245

250

255

gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc 874

Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu

260

265

270

275

ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg 922

Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu

280

285

290

acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat 970

Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn

295

300

305

cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg 1018

Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val

310

315

320

tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt 1066

Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser

325

330

335

ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag 1114

Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys

340 345 350 355  
 ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg 1162  
 Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met  
 360 365 370

aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca 1210  
 Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro  
 375 380 385

ggg cca gag aag gag aac tagggcaagt ggctgtgaga ccctagagac 1258  
 Gly Pro Glu Lys Glu Asn  
 390

cagcgaaggg agaagttggg aagctacgtt ctgttggcca ccagacttgc atttcagcct 1318

ctgtcataat gctctgcct cctcccccg aagttctctg tggatgatgac cgctctcccc 1378

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ccctagtgtc ccttcagcct gggctgacca gtgccccct ctgggcttga ccagttccca 1738







Trp Trp Asn Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn  
305 310 315 320

Arg Ala Val Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu  
325 330 335

Leu Val Ser Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly  
340 345 350

His Ile Lys Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala  
355 360 365

Asp Ala Met Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu  
370 375 380

Leu Val Pro Gly Pro Glu Lys Gln Asn  
385 390

<210> 46

<211> 2396

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50)..(1228)

<400> 46







215

220

225

gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act 778  
Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr

230

235

240

gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att 826  
Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile

245

250

255

gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc 874  
Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu

260

265

270

275

ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg 922  
Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu

280

285

290

acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat 970  
Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn

295

300

305

cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg 1018  
Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val

310

315

320

tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt 1066  
Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser

325

330

335

ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag 1114  
 Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys  
 340 345 350 355

ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg 1162  
 Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met  
 360 365 370

aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca 1210  
 Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro  
 375 380 385

ggg cca gag aag cag aac tagggcaagt ggctgtgaga ccctagagac 1258  
 Gly Pro Glu Lys Gln Asn  
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cagcgaaggg agaagttggg aagctacgtt ctgttgcca ccagacttgc atttcagcct 1318

ctgtcataat gctctgccct cctcccccg aagttctctg tggatgatgac cgctctcccc 1378

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ccctgcccaag gcgacaggga gggcagagg gaggccggt gcttctgcc cccacccttt 1498

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gtctgtttct tgtactggga ccaaagtaaa aatccaagca cattcccctt gcagttaggg 2038

gaggccctac tgcctttctc aagcagagag gcagcttate aaactcagcc caaaactctg 2098

tttacatggg tggggagatg gagcaggga gacagagtg ggatgggtcag gacctgggcc 2158

attgcaacca aatggggac ttcttgggta gggagggtcac tccctctact cactgagcta 2218

ggattaggga gggttattgc cccaaccatt gcaatgggag gtggagggac aggctcagcc 2278

tcctcattgt ctaaagagg cctaaatgtg tgaagtgcga tttctgcttt tgtgtacccc 2338

accaccccat taccacagct gcctttgtgt gtttgtgtca ataaaaagcc aaaccctg 2396

<210> 47

<211> 138



130

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<210> 48

<211> 2976

<212> DNA

<213> Homo sapiens

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<221> CDS

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accctgggct ttccgaggtg ctgtcgccgc tgtccccacc actgcagcc atg atc tcc 118

Met Ile Ser

1

tta acg gac acg cag aaa att gga atg gga tta aca gga ttt gga gtg 166

Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr Gly Phe Gly Val

5

10

15

ttt ttc ctg ttc ttt gga atg att ctc ttt ttt gac aaa gca cta ctg 214

Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe Asp Lys Ala Leu Leu

20

25

30

35

gct att gga aat gtt tta ttt gta gcc ggc ttg gct ttt gta att ggt 262

Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe Val Ile Gly

40

45

50

tta gaa aga aca ttc aga ttc ttc ttc caa aaa cat aaa atg aaa gct 310  
Leu Glu Arg Thr Phe Arg Phe Phe Phe Gln Lys His Lys Met Lys Ala

55

60

65

aca ggt ttt ttt ctg ggt ggt gta ttt gta gtc ctt att ggt tgg cct 358  
Thr Gly Phe Phe Leu Gly Gly Val Phe Val Val Leu Ile Gly Trp Pro

70

75

80

ttg ata ggc atg atc ttc gaa att tat gga ttt ttt ctc ttg ttc agg 406  
Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu Leu Phe Arg

85

90

95

ggc ttc ttt cct gtc gtt gtt ggc ttt att aga aga gtg cca gtc ctt 454  
Gly Phe Phe Pro Val Val Val Gly Phe Ile Arg Arg Val Pro Val Leu

100

105

110

115

gga tcc ctc cta aat tta cct gga att aga tca ttt gta gat aaa gtt 502  
Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val Asp Lys Val

120

125

130

gga gaa agc aac aat atg gta taacaacaag tgaatttgaa gactcattta 553  
Gly Glu Ser Asn Asn Met Val

135

aaatattgtg ttatttataa agtcatttga agaattattca gcacaaaatt aaattacatg 613

aaatagcttg taatgttctt tacaggagtt taaaacgtat agcctacaaa gtaccagcag 673









.. .. .

1 5 10 15

His Ala Phe Leu Lys Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln  
20 25 30

Ser Leu Val Glu Leu Leu Ile Arg Pro Val Gln Arg Leu Pro Ser Val  
35 40 45

Ala Leu Leu Leu Asn Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro  
50 55 60

Asp Lys Ser Thr Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met  
65 70 75 80

Thr His Ile Asn Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile  
85 90 95

Phe Asp Val Val Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser  
100 105 110

Ser His Arg Ser Leu Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu  
115 120 125

His Pro Cys Asp Arg Gly Glu Gln Val Thr Leu Phe Leu Phe Asn Asp  
130 135 140

Cys Leu Glu Ile Ala Arg Lys Arg His Lys Val Ile Gly Thr Phe Arg  
145 150 155 160

Ser Pro His Gly Gln Thr Arg Pro Pro Ala Ser Leu Lys His Ile His  
165 170 175

Leu Met Pro Leu Ser Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr  
180 185 190

Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu  
195 200 205

Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro  
210 215 220

Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val Ala Asn Thr Ile  
225 230 235 240

Cys Lys Ala Asp Ala Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser  
245 250 255

Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu Ser Arg Ala Ser  
260 265 270

Arg Ala Ile Lys Lys Thr Ser Lys Lys Val Thr Arg Ala Phe Ser Phe  
275 280 285

Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu Met Thr Ser His  
290 295 300

Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp Lys His Val Met  
305 310 315 320

Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile Pro Ser Pro Ser  
 325 330 335

Leu Val Ser Leu Pro Ser Phe Phe Glu Arg Arg Ser His Thr Leu Ser  
 340 345 350

Arg Ser Thr Thr His Leu Ile  
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<211> 2636

<212> DNA

<213> Homo sapiens

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aacgtggtgg acctatcctt gcaccagagg agattaagac tattttttggt agcatcccag 180

atatctttga tgtacacact aagataaagg atgatcttga agaccttata gttaattggg 240

atgagagcaa aagcattggt gacatttttc tgaaatattc aaaagatttg gtaaaaacct 300

accctccctt tgtaaacttc ttigaa atg agc aag gaa aca att att aaa tgt 353

Met Ser Lys Glu Thr Ile Ile Lys Cys

1

5

gaa aaa cag aaa cca aga ttt cat gct ttt ctc aag ata aac caa gca 401

Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu Lys Ile Asn Gln Ala

10

15

20

25

aaa cca gaa tgt gga cgg cag agc ctt gtt gaa ctt ctt atc cga cca 449

Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu Leu Leu Ile Arg Pro

30

35

40

gta cag agg tta ccc agt gtt gca tta ctt tta aat gat ctt aag aag 497

Val Gln Arg Leu Pro Ser Val Ala Leu Leu Leu Asn Asp Leu Lys Lys

45

50

55

cat aca gct gat gaa aat cca gac aaa agc act tta gaa aaa gct att 545

His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr Leu Glu Lys Ala Ile

60

65

70

gga tca ctg aag gaa gta atg acg cat att aat gag gat aag aga aaa 593

Gly Ser Leu Lys Glu Val Met Thr His Ile Asn Glu Asp Lys Arg Lys

75

80

85

aca gaa gct caa aag caa att ttt gat gtt gtt tat gaa gta gat gga 641

Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val Tyr Glu Val Asp Gly

90

95

100

105





Met Thr Ser Asp Glu Leu Pro Lys Glu Asn Trp Leu Lys Met Leu Cys  
220 225 230

cga cat gta gct aac acc att tgt aaa gca gat gct gag aat ctt att 1073  
Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp Ala Glu Asn Leu Ile  
235 240 245

tat act gct gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac 1121  
Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp  
250 255 260 265

agt aca ttg agt aga gca tca aga gca ata aaa aag act tca aaa aag 1169  
Ser Thr Leu Ser Arg Ala Ser Arg Ala Ile Lys Lys Thr Ser Lys Lys  
270 275 280

gtt aca aga gca ttc tct ttc tcc aaa act cca aaa aga gct ctt cga 1217  
Val Thr Arg Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg  
285 290 295

agg gct ctt atg aca tcc cac ggc tca gtg gag gga aga agt cct tcc 1265  
Arg Ala Leu Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser  
300 305 310

agc aat gat aag cat gta atg agt cgt ctt tct agc aca tca tca tta 1313  
Ser Asn Asp Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu  
315 320 325

gca ggt atc cct tct ccc tcc ctt gtc agc ctt cct tcc ttc ttt gaa 1361  
147/735



gaaacattgt atattttgca aaaacaagat gttttagct gtttcagaga gactacggt 2123

tatttatggt aattttatcc actagcaaat cttgatttag ttgatagtg tgtggaattt 2183

tattttgaag gataagacca tgggaaaatt gtggtaaaga ctgtttgtac ccttcatgaa 2243

ataattctga agttgccatc agttttacta atcttctgtg aaatgcatag atatgcgcat 2303

gttcaacttt ttattgtggt cttataatta aatgtaaaat tgaaaattca ttgctgttt 2363

caaagtgtga tatctttcac aatagccttt ttatagtcag taattcagaa taatcaagtt 2423

catatggata aatgcatttt tatttcctat ttcttttaggg agtgctacaa atgtttgtca 2483

cttaaatttc aagtttctgt tttaatagtt aactgactat agattgtttt ctatgcatg 2543

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agtaagaact ttgtaaataa atacctaaaa ccc 2636

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<211> 883

<212> PRT

<213> Homo sapiens

<400> 51

Met Ala Glu Asn Ser Val Leu Thr Ser Thr Thr Gly Arg Thr Ser Leu

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Tyr Leu Tyr Glu Lys Ala Asn Thr Pro Glu Leu Lys Lys Ser Val Ser

325

330

335

Met Leu Ser Leu Asn Thr Pro Asn Ser Asn Arg Lys Arg Arg Arg Leu

340

345

350

Lys Glu Thr Leu Ala Gln Leu Ser Arg Asp Thr Asp Val Ser Pro Phe

355

360

365

Pro Pro Arg Lys Arg Pro Ser Ala Glu His Ser Leu Ser Ile Gly Ser

370

375

380

Leu Leu Asp Ile Ser Asn Thr Pro Glu Ser Ser Ile Asn Tyr Gly Asp

385

390

395

400

Thr Pro Lys Ser Cys Thr Lys Ser Ser Lys Ser Ser Thr Pro Val Pro

405

410

415

Ser Lys Gln Ser Ala Arg Trp Gln Val Ala Lys Glu Leu Tyr Gln Thr

420

425

430

Glu Ser Asn Tyr Val Asn Ile Leu Ala Thr Ile Ile Gln Leu Phe Gln

435

440

445

Val Pro Leu Glu Glu Glu Gly Gln Arg Gly Gly Pro Ile Leu Ala Pro

450

455

460

Glu Glu Ile Lys Thr Ile Phe Gly Ser Ile Pro Asp Ile Phe Asp Val

465

470

475

480

His Thr Lys Ile Lys Asp Asp Leu Glu Asp Leu Ile Val Asn Trp Asp  
485 490 495

Glu Ser Lys Ser Ile Gly Asp Ile Phe Leu Lys Tyr Ser Lys Asp Leu  
500 505 510

Val Lys Thr Tyr Pro Pro Phe Val Asn Phe Phe Glu Met Ser Lys Glu  
515 520 525

Thr Ile Ile Lys Cys Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu  
530 535 540

Lys Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu  
545 550 555 560

Leu Leu Ile Arg Pro Val Gln Arg Leu Pro Ser Val Ala Leu Leu Leu  
565 570 575

Asn Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr  
580 585 590

Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met Thr His Ile Asn  
595 600 605

Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val  
610 615 620

Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser  
153/735







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tcc act act ggg agg act agc ttg gca gac tct tcc att ttt gat tct 100  
Ser Thr Thr Gly Arg Thr Ser Leu Ala Asp Ser Ser Ile Phe Asp Ser  
10 15 20

aaa gtt act gag att tcc aag gaa aac tta ctt att gga tct act tca 148  
Lys Val Thr Glu Ile Ser Lys Glu Asn Leu Leu Ile Gly Ser Thr Ser  
25 30 35 40

tat gta gaa gaa gag atg cct cag att gaa aca aga gtg ata ttg gtt 196  
Tyr Val Glu Glu Glu Met Pro Gln Ile Glu Thr Arg Val Ile Leu Val  
45 50 55

caa gaa gct gga aaa caa gaa gaa ctt aca aaa gcc tta aag gac att 244  
Gln Glu Ala Gly Lys Gln Glu Glu Leu Thr Lys Ala Leu Lys Asp Ile  
60 65 70

aaa gtg ggc ttt gta aag atg gag tca gtg gaa gaa ttt gaa ggt ttg 292  
Lys Val Gly Phe Val Lys Met Glu Ser Val Glu Glu Phe Glu Gly Leu  
75 80 85

gat tct ccg gaa ttt gaa aat gta ttt gta gtc acg gac ttt cag gat 340  
Asp Ser Pro Glu Phe Glu Asn Val Phe Val Val Thr Asp Phe Gln Asp  
156/735



gaa agg cgg aat gaa cag gat ttc tat gca gca gtt gat gac ttt aga 724

Glu Arg Arg Asn Glu Gln Asp Phe Tyr Ala Ala Val Asp Asp Phe Arg

220

225

230

aat gaa ttt aaa gtt cct cca ttt caa gat tgt att ttt agt ttc ctg 772

Asn Glu Phe Lys Val Pro Pro Phe Gln Asp Cys Ile Phe Ser Phe Leu

235

240

245

gga ttt tca gat gaa gag aaa acc aat atg gaa gaa atg act gaa atg 820

Gly Phe Ser Asp Glu Glu Lys Thr Asn Met Glu Glu Met Thr Glu Met

250

255

260

caa gga ggt aaa tat tta ccg ctt gga gat gaa aga tgc act cac ctt 868

Gln Gly Gly Lys Tyr Leu Pro Leu Gly Asp Glu Arg Cys Thr His Leu

265

270

275

280

gta gtt gaa gag aat ata gta aaa gat ctt ccc ttt gaa cct tca aag 916

Val Val Glu Glu Asn Ile Val Lys Asp Leu Pro Phe Glu Pro Ser Lys

285

290

295

aaa ctt tat gtt gtc aag caa gag tgg ttc tgg gga agc att caa atg 964

Lys Leu Tyr Val Val Lys Gln Glu Trp Phe Trp Gly Ser Ile Gln Met

300

305

310

gat gcc cga gct gga gaa act atg tat tta tat gaa aag gca aat act 1012

Asp Ala Arg Ala Gly Glu Thr Met Tyr Leu Tyr Glu Lys Ala Asn Thr

315

320

325

cct gag ctc aag aaa tca gtg tca atg ctt tct cta aat acc cct aac 1060

Pro Glu Leu Lys Lys Ser Val Ser Met Leu Ser Leu Asn Thr Pro Asn

330

335

340

agc aat cgc aaa cga cgt cgt tta aaa gaa aca ctt gct cag ctt tca 1108

Ser Asn Arg Lys Arg Arg Arg Leu Lys Glu Thr Leu Ala Gln Leu Ser

345

350

355

360

aga gat aca gac gtg tca cca ttt cca ccc cgt aag cgc cca tca gct 1156

Arg Asp Thr Asp Val Ser Pro Phe Pro Pro Arg Lys Arg Pro Ser Ala

365

370

375

gag cat tcc ctt tcc ata ggg tca ctc cta gat atc tcc aac aca cca 1204

Glu His Ser Leu Ser Ile Gly Ser Leu Leu Asp Ile Ser Asn Thr Pro

380

385

390

gag tct agc att aac tat gga gac acc cca aag tct tgt act aag tct 1252

Glu Ser Ser Ile Asn Tyr Gly Asp Thr Pro Lys Ser Cys Thr Lys Ser

395

400

405

tct aaa agc tcc act cca gtt cct tca aag cag tca gca agg tgg caa 1300

Ser Lys Ser Ser Thr Pro Val Pro Ser Lys Gln Ser Ala Arg Trp Gln

410

415

420

gtt gca aaa gag ctt tat caa act gaa agt aat tat gtt aat ata ttg 1348

Val Ala Lys Glu Leu Tyr Gln Thr Glu Ser Asn Tyr Val Asn Ile Leu

425

430

435

440

gca aca att att cag tta ttt caa gta cca ttg gaa gag gaa gga caa 1396

Ala Thr Ile Ile Gln Leu Phe Gln Val Pro Leu Glu Glu Glu Gly Gln

445

450

455

cgt ggt gga cct atc ctt gca cca gag gag att aag act att ttt ggt 1444

Arg Gly Gly Pro Ile Leu Ala Pro Glu Glu Ile Lys Thr Ile Phe Gly

460

465

470

agc atc cca gat atc ttt gat gta cac act aag ata aag gat gat ctt 1492

Ser Ile Pro Asp Ile Phe Asp Val His Thr Lys Ile Lys Asp Asp Leu

475

480

485

gaa gac ctt ata gtt aat tgg gat gag agc aaa agc att ggt gac att 1540

Glu Asp Leu Ile Val Asn Trp Asp Glu Ser Lys Ser Ile Gly Asp Ile

490

495

500

ttt ctg aaa tat tca aaa gat ttg gta aaa acc tac cct ccc ttt gta 1588

Phe Leu Lys Tyr Ser Lys Asp Leu Val Lys Thr Tyr Pro Pro Phe Val

505

510

515

520

aac ttc ttt gaa atg agc aag gaa aca att att aaa tgt gaa aaa cag 1636

Asn Phe Phe Glu Met Ser Lys Glu Thr Ile Ile Lys Cys Glu Lys Gln

525

530

535

aaa cca aga ttt cat gct ttt ctc aag ata aac caa gca aaa cca gaa 1684

Lys Pro Arg Phe His Ala Phe Leu Lys Ile Asn Gln Ala Lys Pro Glu

540

545

550

tgt gga cgg cag agc ctt gtt gaa ctt ctt atc cga cca gta cag agg 1732

Cys Gly Arg Gln Ser Leu Val Glu Leu Leu Ile Arg Pro Val Gln Arg

tta ccc agt gtt gca tta ctt tta aat gat ctt aag aag cat aca gct 1780  
 Leu Pro Ser Val Ala Leu Leu Leu Asn Asp Leu Lys Lys His Thr Ala  
 gat gaa aat cca gac aaa agc act tta gaa aaa gct att gga tca ctg 1828  
 Asp Glu Asn Pro Asp Lys Ser Thr Leu Glu Lys Ala Ile Gly Ser Leu  
 aag gaa gta atg acg cat att aat gag gat aag aga aaa aca gaa gct 1876  
 Lys Glu Val Met Thr His Ile Asn Glu Asp Lys Arg Lys Thr Glu Ala  
 caa aag caa att ttt gat gtt gtt tat gaa gta gat gga tgc cca gct 1924  
 Gln Lys Gln Ile Phe Asp Val Val Tyr Glu Val Asp Gly Cys Pro Ala  
 aat ctt tta tct tct cac cga agc tta gta cag cgg gtt gaa aca att 1972  
 Asn Leu Leu Ser Ser His Arg Ser Leu Val Gln Arg Val Glu Thr Ile  
 tct cta ggt gag cac ccc tgt gac aga gga gaa caa gta act ctc ttc 2020  
 Ser Leu Gly Glu His Pro Cys Asp Arg Gly Glu Gln Val Thr Leu Phe  
 ctc ttc aat gat tgc cta gag ata gca aga aaa cgg cac aag gtt att 2068  
 Leu Phe Asn Asp Cys Leu Glu Ile Ala Arg Lys Arg His Lys Val Ile

ggc act ttt agg agt cct cat ggc caa acc cga ccc cca gct tct ctt 2116

Gly Thr Phe Arg Ser Pro His Gly Gln Thr Arg Pro Pro Ala Ser Leu

685

690

695

aag cat att cac cta atg cct ctt tct cag att aag aag gta ttg gac 2164

Lys His Ile His Leu Met Pro Leu Ser Gln Ile Lys Lys Val Leu Asp

700

705

710

ata aga gag aca gaa gat tgc cat aat gct ttt gcc ttg ctt gtg agg 2212

Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg

715

720

725

cca cca aca gag cag gca aat gtg cta ctc agt ttc cag atg aca tca 2260

Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser

730

735

740

gat gaa ctt cca aaa gaa aac tgg cta aag atg ctg tgt cga cat gta 2308

Asp Glu Leu Pro Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val

745

750

755

760

gct aac acc att tgt aaa gca gat gct gag aat ctt att tat act gct 2356

Ala Asn Thr Ile Cys Lys Ala Asp Ala Glu Asn Leu Ile Tyr Thr Ala

765

770

775

gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac agt aca ttg 2404

Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu

780

785

790



agt aga gca tca aga gca ata aaa aag act tca aaa aag gtt aca aga 2452

Ser Arg Ala Ser Arg Ala Ile Lys Lys Thr Ser Lys Lys Val Thr Arg

795

800

805

gca ttc tct ttc tcc aaa act cca aaa aga gct ctt cga agg gct ctt 2500

Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu

810

815

820

atg aca tcc cac ggc tca gtg gag gga aga agt cct tcc agc aat gat 2548

Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp

825

830

835

840

aag cat gta atg agt cgt ctt tct agc aca tca tca tta gca ggt atc 2596

Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile

845

850

855

cct tct ccc tcc ctt gtc agc ctt cct tcc ttc ttt gaa agg aga agt 2644

Pro Ser Pro Ser Leu Val Ser Leu Pro Ser Phe Phe Glu Arg Arg Ser

860

865

870

cat acg tta agt aga tct aca act cat ttg ata tgaagcgtta ccaaaatctt 2697

His Thr Leu Ser Arg Ser Thr Thr His Leu Ile

875

880

aaattataga aatgtataga cacctcatat tcaaataaga aactgactta aatgggtactt 2757

gtaattagca cttggtgaaa gctggaagga agataaataa cactaaacta tgctatttga 2817

tttttcttct tgaaagagta aggtttacct gttacathtt caagttaatt catgtaaaaa 2877

atgataatgga ttttgatgta atttatctct tgtttgaatc tgtcattcaa aggccaataa 2937

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aaaatatttt tgcaaattga gataaggaca gaaagattga gaaacattgt atattttgca 3357

aaaacaagat gtttgtagct gtttcagaga gagtacggta tatttatggt aattttatcc 3417

actagcaaat ctigatttag tttgatagtg tgtggaattt tattttgaag gataagacca 3477

tgggaaaatt gtggtaaaga ctgtttgtac ccttcatgaa ataattctga agttgccatc 3537

agttttacta atcttctgtg aaatgcatag atatgcgcac gttcaacttt ttattgtggt 3597

cttataatta aatgtaaaat tgaaaattca tttgctgttt caaagtgtga tatctttcac 3657

aatagccttt ttatagtcag taattcagaa taatcaagtt catatggata aatgcatttt 3717



Glu Asn Val Ser Leu Leu His Trp Ala Ala Ile Asn Asn Arg Leu Asp

85

90

95

Leu Val Lys Phe Tyr Ile Ser Lys Gly Ala Val Val Asp Gln Leu Gly

100

105

110

Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala Ile Arg Gln Gly His

115

120

125

Leu Pro Met Val Ile Leu Leu Leu Gln His Gly Ala Asp Pro Thr Leu

130

135

140

Ile Asp Gly Glu Gly Phe Ser Ser Ile His Leu Ala Val Leu Phe Gln

145

150

155

160

His Met Pro Ile Ile Ala Tyr Leu Ile Ser Lys Gly Gln Ser Val Asn

165

170

175

Met Thr Asp Val Asn Gly Gln Thr Pro Leu Met Leu Ser Ala His Lys

180

185

190

Val Ile Gly Pro Glu Pro Thr Gly Phe Leu Leu Lys Phe Asn Pro Ser

195

200

205

Leu Asn Val Val Asp Lys Ile His Gln Asn Thr Pro Leu His Trp Ala

210

215

220

Val Ala Ala Gly Asn Val Asn Ala Val Asp Lys Leu Leu Glu Ala Gly

166/735

225 230 235 240

Ser Ser Leu Asp Ile Gln Asn Val Lys Gly Glu Thr Pro Leu Asp Met

245 250 255

Ala Leu Gln Asn Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu

260 265 270

Ala Lys Met Arg Ala Asn Gln Lys Phe Arg Leu Trp Arg Trp Leu Gln

275 280 285

Lys Cys Glu Leu Phe Leu Leu Leu Met Leu Ser Val Ile Thr Met Trp

290 295 300

Ala Ile Gly Tyr Ile Leu Asp Phe Asn Ser Asp Ser Trp Leu Leu Lys

305 310 315 320

Gly Cys Leu Leu Val Thr Leu Phe Phe Leu Thr Ser Leu Phe Pro Arg

325 330 335

Phe Leu Val Gly Tyr Lys Asn Leu Val Tyr Leu Pro Thr Ala Phe Leu

340 345 350

Leu Ser Ser Val Phe Trp Ile Phe Met Thr Trp Phe Ile Leu Phe Phe

355 360 365

Pro Asp Leu Ala Gly Ala Pro Phe Tyr Phe Ser Phe Ile Phe Ser Ile

370 375 380











215	220	225	
aat gtt aat gca gtt gat aag ctt ttg gaa gct ggt tct agc ctg gat 835			
Asn Val Asn Ala Val Asp Lys Leu Leu Glu Ala Gly Ser Ser Leu Asp			
230	235	240	
atc cag aat gtt aag gga gaa aca cct ctt gat atg gct cta caa aac 883			
Ile Gln Asn Val Lys Gly Glu Thr Pro Leu Asp Met Ala Leu Gln Asn			
245	250	255	260
aaa aat cag ctc att att cat atg cta aaa aca gaa gcc aaa atg aga 931			
Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu Ala Lys Met Arg			
	265	270	275
gcc aac caa aag ttc aga ctt tgg agg tgg ctg cag aaa tgc gag ctc 979			
Ala Asn Gln Lys Phe Arg Leu Trp Arg Trp Leu Gln Lys Cys Glu Leu			
	280	285	290
ttc ctg ctg ctg atg ctt tct gtg att acc atg tgg gct att gga tac 1027			
Phe Leu Leu Leu Met Leu Ser Val Ile Thr Met Trp Ala Ile Gly Tyr			
	295	300	305
ata ttg gac ttc aat tca gat tct tgg ctt tta aaa gga tgt ctt cta 1075			
Ile Leu Asp Phe Asn Ser Asp Ser Trp Leu Leu Lys Gly Cys Leu Leu			
	310	315	320
gta aca ctg ttt ttt ctg aca tct ttg ttt cca agg ttc ttg gtt ggg 1123			
Val Thr Leu Phe Phe Leu Thr Ser Leu Phe Pro Arg Phe Leu Val Gly			
325	330	335	340



gat caa cac tgc ctg tgg act gga cgg tgc ata ggt ttt ggc aac cat 1507

Asp Gln His Cys Leu Trp Thr Gly Arg Cys Ile Gly Phe Gly Asn His

455

460

465

cac tat tac ata ttc ttc ttg ttt ttc ctt tcc atg gta tgt ggc tgg 1555

His Tyr Tyr Ile Phe Phe Leu Phe Phe Leu Ser Met Val Cys Gly Trp

470

475

480

att ata tat gga tct ttc atc tat ttg tcc agt cat tgt gcc aca aca 1603

Ile Ile Tyr Gly Ser Phe Ile Tyr Leu Ser Ser His Cys Ala Thr Thr

485

490

495

500

ttc aaa gaa gat gga tta tgg act tac ctc aat cag att gtg gcc tgt 1651

Phe Lys Glu Asp Gly Leu Trp Thr Tyr Leu Asn Gln Ile Val Ala Cys

505

510

515

tcc cct tgg gtt tta tat atc ttg atg cta gca act ttc cat ttc tca 1699

Ser Pro Trp Val Leu Tyr Ile Leu Met Leu Ala Thr Phe His Phe Ser

520

525

530

tgg tca aca ttt tta tta tta aat caa ctc ttt cag att gcc ttt ctg 1747

Trp Ser Thr Phe Leu Leu Leu Asn Gln Leu Phe Gln Ile Ala Phe Leu

535

540

545

ggc ctg acc tcc cat gag aga atc agc ctg cag aag cag agc aag cat 1795

Gly Leu Thr Ser His Glu Arg Ile Ser Leu Gln Lys Gln Ser Lys His

550

555

560

atg aaa cag acg ttg tcc ctc agg aag aca cca tac aat ctt gga ttc 1843



aaaaaattttt tttttgt

2426

<210> 55

<211> 257

<212> PRT

<213> Homo sapiens

<400> 55

Met	Ala	Ser	Lys	Ile	Gly	Ser	Arg	Arg	Trp	Met	Leu	Gln	Leu	Ile	Met
1				5					10					15	

Gln	Leu	Gly	Ser	Val	Leu	Leu	Thr	Arg	Cys	Pro	Phe	Trp	Gly	Cys	Phe
			20					25					30		

Ser	Gln	Leu	Met	Leu	Tyr	Ala	Glu	Arg	Ala	Glu	Ala	Arg	Arg	Lys	Pro
			35					40					45		

Asp	Ile	Pro	Val	Pro	Tyr	Leu	Tyr	Phe	Asp	Met	Gly	Ala	Ala	Val	Leu
		50					55					60			

Cys	Ala	Ser	Phe	Met	Ser	Phe	Gly	Val	Lys	Arg	Arg	Trp	Phe	Ala	Leu
		65					70					75			80

Gly	Ala	Ala	Leu	Gln	Leu	Ala	Ile	Ser	Thr	Tyr	Ala	Ala	Tyr	Ile	Gly
				85						90				95	

Gly	Tyr	Val	His	Tyr	Gly	Asp	Trp	Leu	Lys	Val	Arg	Met	Tyr	Ser	Arg
								100				105			110

Thr Val Ala Ile Ile Gly Gly Phe Leu Val Leu Ala Ser Gly Ala Gly

115

120

125

Glu Leu Tyr Arg Arg Lys Pro Arg Ser Arg Ser Leu Gln Ser Thr Gly

130

135

140

Gln Val Phe Leu Gly Ile Tyr Leu Ile Cys Val Ala Tyr Ser Leu Gln

145

150

155

160

His Ser Lys Glu Asp Arg Leu Ala Tyr Leu Asn His Leu Pro Gly Gly

165

170

175

Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu Ala Leu

180

185

190

Ala Phe Leu Ser Gly Tyr Tyr Val Thr Leu Ala Ala Gln Ile Leu Ala

195

200

205

Val Leu Leu Pro Pro Val Met Leu Leu Ile Asp Gly Asn Val Ala Tyr

210

215

220

Trp His Asn Thr Arg Arg Val Glu Phe Trp Asn Gln Met Lys Leu Leu

225

230

235

240

Gly Glu Ser Val Gly Ile Phe Gly Thr Ala Val Ile Leu Ala Thr Asp

245

250

255

Gly









Gly Gly Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu  
175 180 185 190

gcc ctg gcc ttt ctg tca ggc tac tac gtg acc ctc gct gcc cag atc 627  
Ala Leu Ala Phe Leu Ser Gly Tyr Tyr Val Thr Leu Ala Ala Gln Ile  
195 200 205

ctg gct gta ctg ctg ccc cct gtc atg ctg ctc att gat ggc aat gtt 675  
Leu Ala Val Leu Leu Pro Pro Val Met Leu Leu Ile Asp Gly Asn Val  
210 215 220

gct tac tgg cac aac acg cgg cgt gtt gag ttc tgg aac cag atg aag 723  
Ala Tyr Trp His Asn Thr Arg Arg Val Glu Phe Trp Asn Gln Met Lys  
225 230 235

ctc ctt gga gag agt gtg ggc atc ttc gga act gct gtc atc ctg gcc 771  
Leu Leu Gly Glu Ser Val Gly Ile Phe Gly Thr Ala Val Ile Leu Ala  
240 245 250

act gat ggc tgagttttat ggcaagaggc tgagatgggc acagggagcc 820

Thr Asp Gly

255

actgagggtc accctgcctt cctccttgct ggcccagctg ctgtttatTT atgctttttg 880

gtctgtttgt ttgatctttt gcttttttaa aattgttttt tgcagttaag aggcagctca 940

tttgtccaaa tttctgggct cagcgcttgg gagggcagga gccctggcac taatgctgta 1000

caggtttttt tcctgttagg agagctgagg ccagctgccc actgagtctc ctgtccctga 1060

gaagggagta tggcagggct gggatgcggc tactgagagt gggagagtgg gagacagagg 1120

aaggaagatg gagattggaa gtgagcaaat gtgaaaaatt cctctttgaa cctggcagat 1180

gcagctaggc tctgcagtgc tgtttggaga ctgtgagagg gagtgtgtgt gttgacacat 1240

gtggatcagg cccaggaagg gcacaggggc tgagcactac agaagtcaca tgggttctca 1300

gggtatgcca ggggcagaaa cagtaccggc tctctgtcac tcaccttgag agtagagcag 1360

accctgttct gctctgggct gtgaaggggt ggagcaggca gtggccagct ttgcccttcc 1420

tgctgtctct gtttctagct ccatggttgg cctgggtgggg gtggagttcc ctcccaaaca 1480

ccagaccaca cagtcctcca aaaataaaca ttttatatag 1520

<210> 57

<211> 107

<212> PRT

<213> Homo sapiens

<400> 57

Met Ala Leu Phe Ala Gly Gly Lys Leu Arg Val His Leu Asp Ile Gln

1

5

10

15

Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys Asp Lys

20

25

30

Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln Val Glu

35

40

45

Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu Arg Phe

50

55

60

Arg Leu Thr Ser Glu Ser Thr Asn Gln Arg Val Leu Trp Trp Ser Ile

65

70

75

80

Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met Arg His

85

90

95

Leu Lys Ser Phe Phe Glu Ala Lys Lys Leu Val

100

105

<210> 58

<211> 1496

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (9).. (329)

<400> 58

ctaccagg atg gct ctc ttc gct ggt ggc aaa ctg cgt gtg cat ctc gac 50



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caaaccattc agatcagcca cttgctgacc ctggttctta aggacacatg acattagtcc 519

aatctttcaa aatcttgtct tagggcttgt gaggaatcag aactaaccca ggactcagtc 579

ctgcttcttt tgccctgagt gattttcctc tgtttttcac taaataagca aatgaaaact 639

ctctccatta ccttctgctt tctctttgtc cacttaagca gtaggtgact ggcatgtgcc 699

acagagcagg cctgcctca ctgtctgctg gtcagttctg ggcttactta atggctttgt 759

gaatgtaaat aaggggcagg tcttgccct agaggattga gatgttttcc tatatcttag 819

aactatTTTT ggataaatta tatatTTTcc ttcttagtag aagtgttact gcctgtaact 879

agctcaaaat accaatgcag tttctgcatt ctgggttttg ttttctttt tttttttttt 939

ttttttgagt ttgctcttg tcgcccagge tggagtgcaa tggcgtgac tcagctcact 999

ggcaacatct gcctcccggg ttcaaatgat tctcctgcct cagtctcctg agtagctggg 1059

attacaggtg cccgccacca cgtcagcta atttttgtat ttttagtaga gatgggggtt 1119

taccatgttg gccaggctgg tcttagactc ctgacctcag ttgateccacc tgcctcagcc 1179

tctgcattca gtttattcac atatTTTTgg taactcccat ggcagctcct aggatttcag 1239

cggctctgtg gccagaaagc aggcaccagg gctgacctca aggccgtatc agagggccaa 1299







Met His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln  
225 230 235 240

Tyr Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe Pro Glu  
245 250 255

Arg Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln Val Glu  
260 265 270

<210> 60

<211> 1916

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (117).. (932)

<400> 60

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gccgccgccg ctgcttcagc ttattccttg tggcctctgc gggtcctgcc tcagcc atg 119

Met

1

atg atc cac ggc ttc cag agc agc cac cgg gat ttc tgc ttc ggg ccc 167

Met Ile His Gly Phe Gln Ser Ser His Arg Asp Phe Cys Phe Gly Pro

5

10

15



gta cct aca aca gat cat ata gat aca gaa aaa ttg aaa gcc aga gaa 551

Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg Glu

130 135 140 145

cag att aag ttt ttt gaa gaa gtt ctc ctt ttt gag gat gaa ctt cat 599

Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu His

150 155 160

gat cat gga gtt tca agc ctg agt gtg aag att aga gta atg cct tct 647

Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro Ser

165 170 175

agc ttt ttc ctg ctg ttg cgg ttt ttc ttg aga att gat ggg gtg ctt 695

Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp Gly Val Leu

180 185 190

atc aga atg aat gac acg aga ctt tac cat gag gct gac aag acc tac 743

Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp Lys Thr Tyr

195 200 205

atg tta cga gaa tat acg tca cga gaa agc aaa att tct agt ttg atg 791

Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser Ser Leu Met

210 215 220 225

cat gtt cca cct tcc ctc ttc acg gaa cct aat gaa ata tcc cag tat 839

His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln Tyr

230 235 240

tta cca ata aag gaa gca gtt tgt gag aag cta ata ttt cca gaa aga 887

Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe Pro Glu Arg

245

250

255

att gat cct aac cca gca gac tca caa aaa agt aca caa gtg gaa 932

Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln Val Glu

260

265

270

taaaatgtga tacaacatat actcactatg gaatctgact ggacaccttg gctatttgta 992

aggggttatt tttattatga gaattaattg ccttgtttat gtacagattt tctgtagcct 1052

taaaggaaaa aaaaataaag atcgttacag gcaggtttca ctcaactgct atttgtactg 1112

tctgtcttca cattcatatt ccagatttat attttctgga gttaaatttg gatgatttct 1172

aaattatcac aaagtgggac ctacagcagta gtgatgtgtg tgtctcatga gcagtgagca 1232

cagtctgcat tcatcatgaa acactatctt ctaccaggag gaggttaatg taaatcacca 1292

aatcccaatg ccttgtagct ttcataggat tcctgatcat gcatgttgat gtactggctc 1352

ttcactttgg gctttctgat gtttattcac acctttggag agttgcaact tgccacatac 1412

gaaattagtc tcatagtgtg gtgaacttca accccaaaat tttaaaaatg tatttcccc 1472

cagttttaaa ttgcctttga aatttaaaaa aaaaaattta gacttagtac cagaaccaa 1532

aatacctaga tttttggaga acttattaca tacatagaaa catgaatatg gtttaccwct 1592

gtgtgtgtgt gtgtgtgtgt gtgtatacag actttttttt ttaacttggt gattcagatg 1652

tcttggtccc tgaatagtcc tagattactt attttgagaa ttgattgtta aaaattacag 1712

ggaattaaaa taattgcctt ttttttttta gagggtaaga gatgggtaga agagtatgcc 1772

tctgaaaatt ttattagttt attccttggtg agaataccaa gaaaatgtgt atttgcccat 1832

tgctaaatat gatatatgcc attttgtatt tatttgtccc aagtgtcttt ttttaagagg 1892

agaataaaca ataaggaatt actg 1916

<210> 61

<211> 219

<212> PRT

<213> Homo sapiens

<400> 61

Met Asn Arg Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Pro Ser

1

5

10

15

Leu Thr Asp Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp

20

25

30

Lys Lys Ile Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln

35

40

45

Ile Lys Lys Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys

50

55

60

Ala Leu Arg Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp  
65 70 75 80

Asn Leu Ala Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile  
85 90 95

Gln Ser Leu Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly  
100 105 110

Val Lys Glu Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile  
115 120 125

Glu Asp Leu Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu  
130 135 140

Ile Gln Glu Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu  
145 150 155 160

Asp Asp Leu Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala  
165 170 175

Asp Glu Asp Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile  
180 185 190

Pro Glu Gly Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val  
195 200 205



Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys Ala Leu Arg  
55 60 65

gtt tta aag caa aag agg atg tat gag cag cag cgg gac aat ctt gcc 297  
Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp Asn Leu Ala  
70 75 80

caa cag tca ttc aac atg gaa caa gcc aat tat acc atc cag tct ttg 345  
Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile Gln Ser Leu  
85 90 95

aag gac acc aag acc acg gtt gat gct atg aaa ctg gga gta aag gaa 393  
Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly Val Lys Glu  
100 105 110 115

atg aag aag gca tac aag caa gtg aag atc gac cag att gag gat tta 441  
Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile Glu Asp Leu  
120 125 130

caa gac cag cta gag gat atg atg gaa gat gca aat gaa atc caa gaa 489  
Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu Ile Gln Glu  
135 140 145

gca ctg agt cgc agt tat ggc acc cca gaa ctg gat gaa gat gat tta 537  
Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu Asp Asp Leu  
150 155 160











Ser Val Ala Leu Phe Tyr Asn Phe Gly Lys Ser Trp Lys Ser Asp Pro

385 390 395 400

Gly Ile Ile Lys Ala Thr Glu Glu Gln Lys Lys Lys Thr Ile Val Glu

405 410 415

Leu Ala Glu Thr Gly Ser Leu Asp Leu Ser Ile Phe Cys Ser Thr Cys

420 425 430

Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly Val Cys Asn Arg

435 440 445

Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val Gly Asn Cys Val

450 455 460

Gly Ala Gly Asn His Arg Tyr Phe Met Gly Tyr Leu Phe Phe Leu Leu

465 470 475 480

Phe Met Ile Cys Trp Met Ile Tyr Gly Cys Ile Ser Tyr Trp Gly Leu

485 490 495

His Cys Glu Thr Thr Tyr Thr Lys Asp Gly Phe Trp Thr Tyr Ile Thr

500 505 510

Gln Ile Ala Thr Cys Ser Pro Trp Met Phe Trp Met Phe Leu Asn Ser

515 520 525

Val Phe His Phe Met Trp Val Ala Val Leu Leu Met Cys Gln Met Tyr

530

535

540

Gln Ile Ser Cys Leu Gly Ile Thr Thr Asn Glu Arg Met Asn Ala Arg

545

550

555

560

Arg Tyr Lys His Phe Lys Val Thr Thr Thr Ser Ile Glu Ser Pro Phe

565

570

575

Asn His Gly Cys Val Arg Asn Ile Ile Asp Phe Phe Glu Phe Arg Cys

580

585

590

Cys Gly Leu Phe Arg Pro Val Ile Val Asp Trp Thr Arg Gln Tyr Thr

595

600

605

Ile Glu Tyr Asp Gln Ile Ser Gly Ser Gly Tyr Gln Leu Val

610

615

620

<210> 64

<211> 2948

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (14).. (1879)

<400> 64

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Met Ala Asp Gly Pro Asp Glu Tyr Asp Thr Glu Ala

1 5 10

ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc caa agc cat 97

Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro Gln Ser His

15 20 25

tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act cat att gat 145

Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr His Ile Asp

30 35 40

gat tac agc aca tgg gac ata gtc aag gct aca caa tat gga ata tat 193

Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Tyr

45 50 55 60

gaa cgc tgt cga gaa ttg gtg gaa gca ggt tat gat gta cgg caa ccg 241

Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro

65 70 75

gac aaa gaa aat gtt acc ctc ctc cat tgg gct gcc atc aat aac aga 289

Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile Asn Asn Arg

80 85 90

ata gat tta gtc aaa tac tat att tcg aaa ggt gct att gtg gat caa 337

Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile Val Asp Gln

95 100 105

ctt gga ggg gac ctg aat tca act cca ttg cac tgg gcc aca aga caa 385

Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala Thr Arg Gln







ccc ctt ggg ata tat ttg gca acc aaa ttc tgg atg tat gtg acg tgg 1105

Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe Trp Met Tyr Val Thr Trp

350

355

360

ttc ttc tgg ttt tgg aat gat ctc aac ttt tta ttt atc cat ctt cca 1153

Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe Leu Phe Ile His Leu Pro

365

370

375

380

ttc ctt gcc aat agt gtt gca ctt ttc tac aat ttt gga aaa tct tgg 1201

Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr Asn Phe Gly Lys Ser Trp

385

390

395

aaa tca gat cca ggg att att aaa gca aca gaa gag caa aag aaa aag 1249

Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr Glu Glu Gln Lys Lys Lys

400

405

410

aca ata gtt gaa ctt gca gag aca gga agt ctg gac ctc agt ata ttc 1297

Thr Ile Val Glu Leu Ala Glu Thr Gly Ser Leu Asp Leu Ser Ile Phe

415

420

425

tgc agt acc tgt ttg ata cga aaa ccg gtg agg tcc aaa cat tgt ggt 1345

Cys Ser Thr Cys Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly

430

435

440

gtg tgc aac cgc tgt ata gca aaa ttt gat cat cat tgc cca tgg gtg 1393

Val Cys Asn Arg Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val

445

450

455

460

ggt aac tgt gta ggt gca ggc aac cat aga tat ttt atg ggc tac cta 1441





ttgtcttcaa aggcaggaga aaataatggt cacaataaaa tgtgctaaca atgttttggt 2469

tctatcagct gttgcaatgc tgatatattt ctagttcagt gaaataattt gtagtaacct 2529

tactctgagg ttttacggtc tgataatgaa gcacttgcac gagtatagta agtcatgttt 2589

tttgtttcaa atttaaaagc cctgctaatt gcatgacaca ccacatagaa tgtatactag 2649

cagatactat ccagtgaagc ataaattaga atttaatttg atgttcaaaa acagttccat 2709

ttttaagggt taagggtgta ttttcaagaa aaggcagaac aaataatgca aaattctcag 2769

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aaataatggc atttaactaa agatggagca tgatctgtgt acatagcaca tgtgaataaa 2889

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<211> 632

<212> PRT

<213> Homo sapiens

<400> 65

Met Gln Arg Glu Glu Gly Phe Asn Thr Lys Met Ala Asp Gly Pro Asp

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Glu Tyr Asp Thr Glu Ala Gly Cys Val Pro Leu Leu His Pro Glu Glu

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Ile Lys Pro Gln Ser His Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly

35

40

45

Arg Lys Thr His Ile Asp Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala

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Thr Gln Tyr Gly Ile Tyr Glu Arg Cys Arg Glu Leu Val Glu Ala Gly

65

70

75

80

Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn Val Thr Leu Leu His Trp

85

90

95

Ala Ala Ile Asn Asn Arg Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys

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105

110

Gly Ala Ile Val Asp Gln Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu

115

120

125

His Trp Ala Thr Arg Gln Gly His Leu Ser Met Val Val Gln Leu Met

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Lys Tyr Gly Ala Asp Pro Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys

145

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160

Ile His Leu Ala Ala Gln Phe Gly His Thr Ser Ile Val Ala Tyr Leu

165

170

175



Gly Val Trp Ala Thr Val Gln Phe Leu Ser Lys Ser Phe Phe Asp His

340

345

350

Ser Met His Ser Ala Leu Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe

355

360

365

Trp Met Tyr Val Thr Trp Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe

370

375

380

Leu Phe Ile His Leu Pro Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr

385

390

395

400

Asn Phe Gly Lys Ser Trp Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr

405

410

415

Glu Glu Gln Lys Lys Lys Thr Ile Val Glu Leu Ala Glu Thr Gly Ser

420

425

430

Leu Asp Leu Ser Ile Phe Cys Ser Thr Cys Leu Ile Arg Lys Pro Val

435

440

445

Arg Ser Lys His Cys Gly Val Cys Asn Arg Cys Ile Ala Lys Phe Asp

450

455

460

His His Cys Pro Trp Val Gly Asn Cys Val Gly Ala Gly Asn His Arg

465

470

475

480

Tyr Phe Met Gly Tyr Leu Phe Phe Leu Leu Phe Met Ile Cys Trp Met







cat att gat gat tac agc aca tgg gac ata gtc aag gct aca caa tat 308

His Ile Asp Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr

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65

gga ata tat gaa cgc tgt cga gaa ttg gtg gaa gca ggt tat gat gta 356

Gly Ile Tyr Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val

70

75

80

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Arg Gln Pro Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile

85

90

95

aat aac aga ata gat tta gtc aaa tac tat att tcg aaa ggt gct att 452

Asn Asn Arg Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile

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105

110

115

gtg gat caa ctt gga ggg gac ctg aat tca act cca ttg cac tgg gcc 500

Val Asp Gln Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala

120

125

130

aca aga caa ggc cat cta tcc atg gtt gtg caa cta atg aaa tat ggt 548

Thr Arg Gln Gly His Leu Ser Met Val Val Gln Leu Met Lys Tyr Gly

135

140

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gca gat cct tca tta att gat gga gaa gga tgt agc tgt att cat ctg 596

Ala Asp Pro Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys Ile His Leu

150

155

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gct gct cag ttc gga cat acc tca att gtt gct tat ctc ata gca aaa 644

Ala Ala Gln Phe Gly His Thr Ser Ile Val Ala Tyr Leu Ile Ala Lys

165 170 175

gga cag gat gta gat atg atg gat cag aat gga atg acg cct tta atg 692

Gly Gln Asp Val Asp Met Met Asp Gln Asn Gly Met Thr Pro Leu Met

180 185 190 195

tgg gca gca tat aga aca cat agt gtg gat cca act aga ttg ctt tta 740

Trp Ala Ala Tyr Arg Thr His Ser Val Asp Pro Thr Arg Leu Leu Leu

200 205 210

aca ttc aat gtt tca gtt aac ctt ggt gac aag tat cac aaa aac act 788

Thr Phe Asn Val Ser Val Asn Leu Gly Asp Lys Tyr His Lys Asn Thr

215 220 225

gct ctg cat tgg gca gtg cta gca ggg aat acc aca gtc att agc ctt 836

Ala Leu His Trp Ala Val Leu Ala Gly Asn Thr Thr Val Ile Ser Leu

230 235 240

ctt ctg gaa gct gga gct aat gtt gat gcc cag aat atc aag ggc gaa 884

Leu Leu Glu Ala Gly Ala Asn Val Asp Ala Gln Asn Ile Lys Gly Glu

245 250 255

tca gcg ctt gat ttg gca aaa cag aga aaa aat gtg tgg atg atc aac 932

Ser Ala Leu Asp Leu Ala Lys Gln Arg Lys Asn Val Trp Met Ile Asn

260 265 270 275

cac tta caa gag gca agg caa gca aaa gga tat gac aat ccg tcc ttc 980

His Leu Gln Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn Pro Ser Phe

280

285

290

ctt aga aag ctg aaa gct gat aag gaa ttt cgg cag aaa gta atg tta 1028  
 Leu Arg Lys Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys Val Met Leu  
 295 300 305

gga act cct ttc cta gtt att tgg ctg gtt ggg ttt ata gca gac cta 1076  
 Gly Thr Pro Phe Leu Val Ile Trp Leu Val Gly Phe Ile Ala Asp Leu  
 310 315 320

aat att gat tct tgg ctc att aaa ggg cta atg tat ggt ggt gtt tgg 1124  
 Asn Ile Asp Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly Gly Val Trp  
 325 330 335

gct aca gta cag ttt ctt tca aaa tcc ttt ttc gat cat tca atg cat 1172  
 Ala Thr Val Gln Phe Leu Ser Lys Ser Phe Phe Asp His Ser Met His  
 340 345 350 355

agt gca ttg ccc ctt ggg ata tat ttg gca acc aaa ttc tgg atg tat 1220  
 Ser Ala Leu Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe Trp Met Tyr  
 360 365 370

gtg acg tgg ttc ttc tgg ttt tgg aat gat ctc aac ttt tta ttt atc 1268  
 Val Thr Trp Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe Leu Phe Ile  
 375 380 385

cat ctt cca ttc ctt gcc aat agt gtt gca ctt ttc tac aat ttt gga 1316  
 His Leu Pro Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr Asn Phe Gly  
 390 395 400



gga ttt tgg aca tac att act cag att gcc acg tgt tca cct tgg atg 1700

Gly Phe Trp Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser Pro Trp Met

520

525

530

ttt tgg atg ttc ctg aac agt gtt ttc cac ttc atg tgg gtg gct gta 1748

Phe Trp Met Phe Leu Asn Ser Val Phe His Phe Met Trp Val Ala Val

535

540

545

tta ctc atg tgt cag atg tac cag ata tca tgt tta ggt att act aca 1796

Leu Leu Met Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly Ile Thr Thr

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aat gaa aga atg aat gcc agg aga tac aag cac ttt aaa gtc aca aca 1844

Asn Glu Arg Met Asn Ala Arg Arg Tyr Lys His Phe Lys Val Thr Thr

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575

acg tct att gaa agc cca ttc aac cat gga tgt gta aga aat att ata 1892

Thr Ser Ile Glu Ser Pro Phe Asn His Gly Cys Val Arg Asn Ile Ile

580

585

590

595

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Asp Phe Phe Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro Val Ile Val

600

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610

gac tgg acc agg cag tat aca ata gaa tat gac caa ata tca gga tct 1988

Asp Trp Thr Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile Ser Gly Ser

615

620

625

ggg tac cag ctg gtg tagcgacatc ttatcctatg aagcatattg ctgagtgggtg 2043













Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala  
245 250 255

Pro Glu Ala Val Thr Val Val Thr Ile Ala Pro Asp Phe His Gly Val  
260 265 270

His His Gly His Ile Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr  
275 280 285

Ser Val Leu Cys Phe Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro  
290 295 300

Gln Leu Val Trp Thr Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu  
305 310 315 320

Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu  
325 330 335

Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu  
340 345 350

Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr  
355 360 365

Met His Glu Tyr Lys Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr  
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His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His Ser His

15 20 25

gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat gga aac agt cct att 147

Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser Pro Ile

30 35 40

ctt tat tac atc gtg gag ctg tct gaa aac aac tct cca tgg aag gtg 195

Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val

45 50 55

cat ctg tca aac gtt ggc cct gag atg aca ggc gtc acc gtg agt ggc 243

His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val Ser Gly

60 65 70

ctg act ccg gct cgt acc tat caa ttc cgg gtg tgc gcg gtg aat gaa 291

Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val Asn Glu

75 80 85 90

gtg ggc agg ggc cag tac agt gcc gag aca agc agg ttg atg cta cct 339

Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met Leu Pro

95

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gaa gaa cca ccc agt gct ccc ccg aaa aat ata gtg gcc agt ggg cgg 387

Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser Gly Arg

110

115

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act aat cag tcc att atg gtc cag tgg cag cca ccc cca gaa aca gag 435

Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu

125

130

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cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc 483

His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly

140

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ctt ccc gga gag tac cag cag cgg aac atc acc agc ccg gag gtg aac 531

Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn

155

160

165

170

tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag 579

Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln

175

180

185

gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc ttc agc agg gca gtg 627

Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg Ala Val

190

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200

acc gag tac acc ttg cag gga gtg ccc acc gcg ccc ccg cag aac gtg 675

Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln Asn Val



205

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215

cag acg gaa gcc gtg aac tcc acc acc att cag ttc ctg tgg aac cct 723  
Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro

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ccg cct cag cag ttt atc aat ggc atc aac cag gga tac aag ctt ctg 771  
Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu

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gca tgg ccg gca gat gcc ccc gag gct gtc act gtg gtc act att gcc 819  
Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr Ile Ala

255

260

265

cca gat ttc cac gga gtc cac cat gga cac ata acg aac ctg aag aag 867  
Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu Lys Lys

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275

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ttt acc gcc tac ttc act tcc gtt ctg tgc ttc acc acc cct ggg gac 915  
Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro Gly Asp

285

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295

ggg cct ccc agc aca cct cag ctg gtc tgg act cag gaa gac aaa cca 963  
Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp Lys Pro

300

305

310

gga gct gtg gga cat ctg agt ttc aca gag atc ttg gac aca tct ctc 1011  
Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu

315

320

325

330



tcc agg tgg att gtt gag ggg cag atg aga cct gaa ggt gtt gga tta 1395  
 Ser Arg Trp Ile Val Glu Gly Gln Met Arg Pro Glu Gly Val Gly Leu  
 445 450 455

cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca 1443  
 Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu Pro Ala  
 460 465 470

aac ctc gga agt ctg tgg ctg ctc agc ctg gtg tat tgg tgt tac agc 1491  
 Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser  
 475 480 485 490

cag aaa ctt tgg gaa ttc tct tgt tagttgggta gttttactgt aattttctat 1545  
 Gln Lys Leu Trp Glu Phe Ser Cys  
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aaagaattca tatcatctgt taatggcgac agtttttggt tcttcctttg aattttttat 1605

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atttcctagg agttgggttt ttttttttta aagcataaat aaatttaatt gcatcag 1902



Val Gln Trp Gln Pro Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg  
130 135 140

Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln  
145 150 155 160

Gln Arg Asn Ile Thr Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp  
165 170 175

Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly  
180 185 190

Ala Gly Leu Gly Val Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln  
195 200 205

Gly Val Pro Thr Ala Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn  
210 215 220

Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile  
225 230 235 240

Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala  
245 250 255

Pro Glu Ala Val Thr Val Val Thr Ile Ala Pro Asp Phe His Gly Val  
260 265 270

His His Gly His Ile Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr  
231/735









Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu  
125 130 135

cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc 483  
His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly  
140 145 150

ctt ccc gga gag tac cag cag cgg aac atc acc agc ccg gag gtg aac 531  
Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn  
155 160 165 170

tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag 579  
Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln  
175 180 185

gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc ttc agc agg gca gtg 627  
Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg Ala Val  
190 195 200

acc gag tac acc ttg cag gga gtg ccc acc gcg ccc ccg cag aac gtg 675  
Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln Asn Val  
205 210 215

cag acg gaa gcc gtg aac tcc acc acc att cag ttc ctg tgg aac cct 723  
Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro  
220 225 230

ccg cct cag cag ttt atc aat ggc atc aac cag gga tac aag ctt ctg 771  
235/735

Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu  
 235 240 245 250

gca tgg ccg gca gat gcc ccc gag gct gtc act gtg gtc act att gcc 819  
 Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr Ile Ala  
 255 260 265

cca gat ttc cac gga gtc cac cat gga cac ata acg aac ctg aag aag 867  
 Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu Lys Lys  
 270 275 280

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 Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro Gly Asp  
 285 290 295

ggg cct ccc agc aca cct cag ctg gtc tgg act cag gaa gac aaa cca 963  
 Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp Lys Pro  
 300 305 310

gga gct gtg gga cat ctg agt ttc aca gag atc ttg gac aca tct ctc 1011  
 Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu  
 315 320 325 330

aag gtc agc tgg cag gag ccc ctg gag aaa aat ggc atc att act ggc 1059  
 Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly  
 335 340 345

tat cag atc tct tgg gaa gtg tac ggc agg aac gac tct cgt ctc acg 1107  
 Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr  
 236/735

350 355 360  
 cac acc ctg aac agc acg acg cac gag tac aag atc caa ggc ctc tca 1155  
 His Thr Leu Asn Ser Thr Thr His Glu Tyr Lys Ile Gln Gly Leu Ser  
 365 370 375

tct ctc acc acc tac acc atc gac gtg gcc gct gtg act gcc gtg ggc 1203  
 Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala Val Gly  
 380 385 390

act ggc ctg gtg act tca tcc acc att tct tct gga gtg ccc cca gac 1251  
 Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro Pro Asp  
 395 400 405 410

ctt cct ggt gcc cca tcc aac ctg gtc att tcc aac atc agc cct cgc 1299  
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 415 420 425

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 Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile  
 430 435 440

tcc agg tgg att gtt gag ggg cag atg aga cat caa ggt gtt gga tta 1395  
 Ser Arg Trp Ile Val Glu Gly Gln Met Arg His Gln Gly Val Gly Leu  
 445 450 455

cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca 1443  
 Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu Pro Ala  
 460 465 470





Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn Gly Lys  
165 170 175

Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile Glu Gly  
180 185 190

Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly Thr Val  
195 200 205

Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile Val Arg  
210 215 220

Lys Arg Trp Arg Leu Val Lys Gln Val Ser His Val Gly Val Leu Gly  
225 230 235 240

Gln Trp Ile Gln Arg  
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<213> Homo sapiens

<220>

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acgctg atg ccc gtg cag ctg tct gag cac ccg gaa tgg aat gag tct 168

Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser

1 5 10

atg cac tcc ctg cgg atc agt gtg ggg ggc ctt cct gtg ctg gcg tcc 216

Met His Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser

15 20 25 30

atg acc aag gcc gcg gac ccc cgc ttc cgc ccc cgc tgg aag gtg atc 264

Met Thr Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile

35 40 45

ctg acg ttc ttt gtg ggt gct gcc atc ctg tgg ctg ctg tgc tcc cac 312

Leu Thr Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His

50 55 60

cgc ccg gcc ccc ggc agg ccc ccc acc cac aat gca cac aac tgg agg 360

Arg Pro Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg

65 70 75

ctc ggc cag gcg ccc gcc aac tgg tac aat gac acc tac ccc ctg tct 408

Leu Gly Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser

80 85 90

ccc cca caa agg aca ccg gct ggg att cgg tat cga atc gca gtt atc 456

Pro Pro Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile  
 95 100 105 110

gca gac ctg gac aca gag tca agg gcc caa gag gaa aac acc tgg ttc 504  
 Ala Asp Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe  
 115 120 125

agt tac ctg aaa aag ggc tac ctg acc ctg tca gac agt ggg gac aag 552  
 Ser Tyr Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys  
 130 135 140

gtg gcc gtg gaa tgg gac aaa gac cat ggg gtc ctg gag tcc cac ctg 600  
 Val Ala Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu  
 145 150 155

gcg gag aag ggg aga ggc atg gag cta tcc gac ctg att gtt ttc aat 648  
 Ala Glu Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn  
 160 165 170

ggg aaa ctc tac tcc gtg gat gac cgg acg ggg gtc gtc tac cag atc 696  
 Gly Lys Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile  
 175 180 185 190

gaa ggc agc aaa gcc gtg ccc tgg gtg att ctg tcc gac ggc gac ggc 744  
 Glu Gly Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly  
 195 200 205

acc gtg gag aaa ggc ttc aag gcc gaa tgg ctg gca gtg cgg gag att 792  
 Thr Val Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile  
 242/735







100

105

110

Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu

115

120

125

Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro

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135

140

Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His

145

150

155

160

Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly

165

170

175

Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly

180

185

190

Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val

195

200

205

Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln

210

215

220

Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp

225

230

235

240

Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe

245

250

255



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tatccttgge gccacagtcg gccaccgggg ctcgccgccg tc atg gag agc gga 114

Met Glu Ser Gly

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ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc acc tct gtg 162

Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val

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gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc 210

Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser

25 30 35

caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag 258

Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys

40 45 50

agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata 306

Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile

55 60 65

gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg 354

Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val

70 75 80

gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag 402

Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys

85 90 95 100

atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc 450

Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile

105

110

115

att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag 498

Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu

120

125

130

gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg 546

Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val

135

140

145

gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tcg att cag 594

Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln

150

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tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa 642

Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys

165

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175

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ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca 690

Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr

185

190

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ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc ctg cag ccg 738

Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro

200

205

210



Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg

325 330 335 340

cag gcg atc acc cgg gtg ata ccc ccg tac aac agc taatagtttg 1168

Gln Ala Ile Thr Arg Val Ile Pro Pro Tyr Asn Ser

345 350

gaagccgcac agcttgacct ggaagcaccc ctgccccctt ttcagggatt tttatctcga 1228

ggcctttgga ggagcagtgg tgggggtagc tgtcacctcc aggtatgatt gagggaggaa 1288

tgggtagaa actctccaga cccatgcctc caatggcagg atgctgcctt tcccacctga 1348

gaggggaccc tgtccatgtg cagcctcacc agagcctcac cctggggagga tgccgtggcg 1408

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caaagccagt gatcagcagc tcttctgttc ctgtgtcttc tgtttttttc tggatgaatcg 1528

ttgcttgctg tggacttggt ggaggactca gaggggagga aaggctgggc cccgagtaca 1588

acggatgcct tgggtgctgc ctccgaagag actctgccgc agcttttctt ctttttcctc 1648

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gagcctttta gtgcaagaca gatggggctg ttttccccca cctctgagta gttggaggtc 2248

acatacacag ctcttttttt attgcccttt tctgcctctg aatgttcatc tctcgtcctc 2308

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<210> 75

<211> 352

<212> PRT

<213> Homo sapiens

<400> 75

Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly

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Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys  
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Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly  
 35 40 45

Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro  
 50 55 60

Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn  
 65 70 75 80

Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu  
 85 90 95

Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp  
 100 105 110

Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu  
 115 120 125

Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro  
 130 135 140

Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His  
 145 150 155 160

Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly  
 252/735

165

170

175

Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly

180

185

190

Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val

195

200

205

Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln

210

215

220

Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp

225

230

235

240

Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe

245

250

255

Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu

260

265

270

Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser

275

280

285

Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val

290

295

300

Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val

305

310

315

320



25

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35

caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag 258

Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys

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agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata 306

Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile

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gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg 354

Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val

70

75

80

gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag 402

Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys

85

90

95

100

atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc 450

Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile

105

110

115

att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag 498

Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu

120

125

130

gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg 546

Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val

135

140

145



aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag 930  
 Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln  
 265 270 275

gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct 978  
 Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro  
 280 285 290

gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc 1026  
 Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser  
 295 300 305

ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc 1074  
 Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr  
 310 315 320

gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct atc tgc aga 1122  
 Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg  
 325 330 335 340

cag gcg atc acc cgg gtg ata ccc ctg tac aac agc taatagtttg 1168  
 Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser  
 345 350

gaagccgcac agcttgacct ggaagcacc ctgccccctt ttcagggatt tttatctcga 1228

ggcctttgga ggagcagtgg tgggggtagc tgtcacctcc aggtatgatt gagggaggaa 1288

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tgaagtcagc acatccgctt ctgcccagat ggteggggcc ccgggcaaca gattgaagag 1828

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gaactcctgc cacttgggag agctcggggt ggteccctggt tttccctcct ggagaatgag 1948

gcgcagaggc ctgcctcct gaaggacgca gtgtggatgc cactggccta gtgtcctggc 2008

ctcacagctt ccttgcaagg ctgtcacaag gaaaagcagc cggttggcac cctgagcata 2068

tgcctcttg gggctccctc atccagcccg tcgcagcttt gacatcttgg tgtactcatg 2128

tcgttctcc ttgtgttacc cctcctcagt attaccattt gccctcacc tgccttggt 2188





Leu Tyr Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser Leu Ser Asn

85

90

95

Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu Asp Asn Ser

100

105

110

Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu Leu Leu

115

120

125

Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg Ile Ser

130

135

140

Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu Phe Leu

145

150

155

160

Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val Glu Lys

165

170

175

Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu Ile Ile

180

185

190

Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu Val Ile Phe

195

200

205

Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys Asn Pro Ile

210

215

220

Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe Leu Asp

260/735

225 230 235 240

Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro Phe Leu

245 250 255

Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala Gly Met

260 265 270

Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr

275 280 285

His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe

290 295 300

Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly Phe His

305 310 315 320

Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His Arg Thr Asp

325 330 335

Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg His Phe

340 345 350

Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu Ala Thr Ala

355 360 365

Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser

370 375 380

Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His Gly Leu Phe  
385 390 395 400

His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile  
405 410 415

Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu  
420 425 430

Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly Met Leu  
435 440 445

Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr Tyr Gly  
450 455 460

Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His Ser Lys  
465 470 475 480

Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg His Asp  
485 490 495

Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly Glu Trp  
500 505 510

Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile Glu Trp  
515 520 525

Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile Val Leu  
530 535 540

Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg Lys Ile Asn  
 545 550 555 560

Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys Thr Val Asp  
 565 570 575

Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr Lys Asp Trp  
 580 585 590

Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp Thr Glu Lys  
 595 600 605

Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg Trp Ser Asp  
 610 615 620

Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys His Trp Met  
 625 630 635 640

Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu Ala Asn Trp  
 645 650 655

Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys Phe Arg Cys  
 660 665 670

Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val Leu Asp Thr  
 675 680 685

Gly Gln Gly Phe Lys Leu Val Lys Ser



tat tta gca atg aca aga ctg gaa gaa gta aat aga gaa gtg aac atg 458  
Tyr Leu Ala Met Thr Arg Leu Glu Glu Val Asn Arg Glu Val Asn Met  
15 20 25

cat tct tca gtg cgg tat ctt ggc tat tta gcc aga atc aat tta ttg 506  
His Ser Ser Val Arg Tyr Leu Gly Tyr Leu Ala Arg Ile Asn Leu Leu  
30 35 40 45

gtt gct ata tgc tta ggt cta tac gta aga tgg gaa aaa aca gca aat 554  
Val Ala Ile Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn  
50 55 60

tcc tta att ttg gta att ttt att ctt ggt ctt ttt gtt ctt gga atc 602  
Ser Leu Ile Leu Val Ile Phe Ile Leu Gly Leu Phe Val Leu Gly Ile  
65 70 75

gcc agc ata ctc tat tac tat ttt tca atg gaa gca gca agt tta agt 650  
Ala Ser Ile Leu Tyr Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser  
80 85 90

ctc tcc aat ctt tgg ttt gga ttc ttg ctt ggc ctc cta tgt ttt ctt 698  
Leu Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu  
95 100 105

gat aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat 746  
Asp Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr  
110 115 120 125

ttg ctt cta aca tcc ata gtg tta agg ata ttg tgc tct ctg gtg gag 794

Leu Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu  
130 135 140

aga att tct ggt tat gtc cgt cat cgg ccc act tta cta acc aca gtt 842  
Arg Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val  
145 150 155

gaa ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg 890  
Glu Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu  
160 165 170

gtg gag aag tct ctg agt gtc att ttg ctt gtt gta gct ctg gct atg 938  
Val Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met  
175 180 185

ctg att att gat ctg aga atg aaa tct ttc tta gct att cca aac tta 986  
Leu Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu  
190 195 200 205

gtt att ttt gca gtt ttg tta ttt ttt tcc tca ttg gaa act ccc aaa 1034  
Val Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys  
210 215 220

aat ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct 1082  
Asn Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro  
225 230 235

ttc ctt gac att tat ttt agt gga ctt tca gta act gaa aga tgg aaa 1130  
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250

265

285

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315

330

345

365

gca aca gcg att ttg gga gca gtt tcc tgg cag cca aca aat gga att 1514

Ala Thr Ala Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile

370

375

380

ttc ttg agc atg ttt cta atc gtt ttg cca ttg gaa tcc atg gct cat 1562

Phe Leu Ser Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His

385

390

395

ggg ctc ttc cat gaa ttg ggt aac tgt tta gga gga aca tct gtt gga 1610

Gly Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly

400

405

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tat gct att gtg att ccc acc aac ttc tgc agt cct gat ggt cag cca 1658

Tyr Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro

415

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425

aca ctg ctt ccc cca gaa cat gta cag gag tta aat ttg agg tct act 1706

Thr Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr

430

435

440

445

ggc atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag 1754

Gly Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu

450

455

460

acc tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg 1802

Thr Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu

465

470

475

cat tcc aaa cta aaa gct ttc ctc gaa ctt cgg aca gtg gat gga ccc 1850  
His Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro  
480 485 490

aga cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca 1898  
Arg His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr  
495 500 505

gga gag tgg gct cta gca ggt gga gat aca cta cgc ctt gac aca ctt 1946  
Gly Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu  
510 515 520 525

ata gaa tgg tgg aga gaa aag aat ggt tcc ttt tgt tcc cgg ctt att 1994  
Ile Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile  
530 535 540

atc gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg 2042  
Ile Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg  
545 550 555

aaa att aat gac cag tat att gca gtg caa gga gca gag ttg ata aaa 2090  
Lys Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys  
560 565 570

aca gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca 2138  
Thr Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr  
575 580 585

aaa gac tgg gta gaa tat aac tgc aac tcc agt aat aac atc tgc tgg 2186

Lys Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp  
 590 595 600 605

act gaa aag gga cgc aca gtg aaa gca gta tat ggt gtg tca aaa cgg 2234  
 Thr Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg  
 610 615 620

tgg agt gac tac act ctg cat ttg cca acg gga agc gat gtg gcc aag 2282  
 Trp Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys  
 625 630 635

cac tgg atg tta cac ttt cct cgt att aca tat ccc cta gtg cat ttg 2330  
 His Trp Met Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu  
 640 645 650

gca aat tgg tta tgc ggt ctg aac ctt ttt tgg atc tgc aaa act tgt 2378  
 Ala Asn Trp Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys  
 655 660 665

ttt agg tgc ttg aaa aga tta aaa atg agt tgg ttt ctt cct act gtg 2426  
 Phe Arg Cys Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val  
 670 675 680 685

ctg gac aca gga caa ggc ttc aaa ctt gtc aaa tct taatttggac 2472  
 Leu Asp Thr Gly Gln Gly Phe Lys Leu Val Lys Ser  
 690 695

cccaaagcgg gatattaata agcactcata ctaccaatta tcactaactt gccatttttt 2532



...and ... ..  
... ..

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185

190

Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr His Leu Trp Tyr Phe Val  
195 200 205

Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe Trp Met Ile Cys His Ile  
210 215 220

Ile Phe Leu Leu Thr Leu Trp Gly Phe His Thr Lys Leu Asn Asp Cys  
225 230 235 240

His Lys Val Tyr Phe Thr His Arg Thr Asp Tyr Asn Ser Leu Asp Arg  
245 250 255

Ile Met Ala Ser Lys Gly Met Arg His Phe Cys Leu Ile Ser Glu Gln  
260 265 270

Leu Val Phe Phe Ser Leu Leu Ala Thr Ala Ile Leu Gly Ala Val Ser  
275 280 285

Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser Met Phe Leu Ile Val Leu  
290 295 300

Pro Leu Glu Ser Met Ala His Gly Leu Phe His Glu Leu Gly Asn Cys  
305 310 315 320

Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile Val Ile Pro Thr Asn Phe  
325 330 335

Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu Pro Pro Glu His Val Gln  
273/735

340

345

350

Glu Leu Asn Leu Arg Ser Thr Gly Met Leu Asn Ala Ile Gln Arg Phe

355

360

365

Phe Ala Tyr His Met Ile Glu Thr Tyr Gly Cys Asp Tyr Ser Thr Ser

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Gly Leu Ser Phe Asp Thr Leu His Ser Lys Leu Lys Ala Phe Leu Glu

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395

400

Leu Arg Thr Val Asp Gly Pro Arg His Asp Thr Tyr Ile Leu Tyr Tyr

405

410

415

Ser Gly His Thr His Gly Thr Gly Glu Trp Ala Leu Ala Gly Gly Asp

420

425

430

Thr Leu Arg Leu Asp Thr Leu Ile Glu Trp Trp Arg Glu Lys Asn Gly

435

440

445

Ser Phe Cys Ser Arg Leu Ile Ile Val Leu Asp Ser Glu Asn Ser Thr

450

455

460

Pro Trp Val Lys Glu Val Arg Lys Ile Asn Asp Gln Tyr Ile Ala Val

465

470

475

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Gln Gly Ala Glu Leu Ile Lys Thr Val Asp Ile Glu Glu Ala Asp Pro

485

490

495



Pro Gln Leu Gly Asp Phe Thr Lys Asp Trp Val Glu Tyr Asn Cys Asn  
500 505 510

Ser Ser Asn Asn Ile Cys Trp Thr Glu Lys Gly Arg Thr Val Lys Ala  
515 520 525

Val Tyr Gly Val Ser Lys Arg Trp Ser Asp Tyr Thr Leu His Leu Pro  
530 535 540

Thr Gly Ser Asp Val Ala Lys His Trp Met Leu His Phe Pro Arg Ile  
545 550 555 560

Thr Tyr Pro Leu Val His Leu Ala Asn Trp Leu Cys Gly Leu Asn Leu  
565 570 575

Phe Trp Ile Cys Lys Thr Cys Phe Arg Cys Leu Lys Arg Leu Lys Met  
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Ser Trp Phe Leu Pro Thr Val Leu Asp Thr Gly Gln Gly Phe Lys Leu  
595 600 605

Val Lys Ser  
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<222> (629).. (2461)

<400> 80

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ggcgtgccgc ctccctgttc tcagtcgcag gctgaagcct tgtctgctct cctccttttt 180

ggtttggttt tggaactgac tccgagggtt gggagagcgc gttggtggcg acggccgagt 240

cagatcacta taaacaaaat ttccacaaga gaaaatgttg aataggagt tgcggataca 300

ttggatatac tggatgaaat acaagcgggt aatttttgta acgtgaggga aaagcccaca 360

ttgctggtta catgtgtaaa tcaactgcgtt attgcttttag tcattgtctc tathtagcaa 420

tgacaagact ggaagaagta aatagagaag tgaacatgca ttcttcagtg cggatatctg 480

ctathtagcc agaatcaatt tattgggtgc tatatgctta ggtctatacg taagatggga 540

aaaaacagca aattccttaa ttttggtaat ttttattctt ggtctttttg ttcttggaat 600

cgccagcata ctctattact atttttca atg gaa gca gca agt tta agt ctc 652

Met Glu Ala Ala Ser Leu Ser Leu

tcc aat ctt tgg ttt gga ttc ttg ctt ggc ctc cta tgt ttt ctt gat 700  
 Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu Asp  
 10 15 20

aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat ttg 748  
 Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu  
 25 30 35 40

ctt cta aca tcc ata gtg tta agg ata ttg tgc tct ctg gtg gag aga 796  
 Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg  
 45 50 55

att tct ggt tat gtc cgt cat cgg ccc act tta cta acc aca gtt gaa 844  
 Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu  
 60 65 70

ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg gtg 892  
 Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val  
 75 80 85

gag aag tct ctg agt gtc att ttg ctt gtt gta gct ctg gct atg ctg 940  
 Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu  
 90 95 100

att att gat ctg aga atg aaa tct ttc tta gct att cca aac tta gtt 988  
 Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu Val  
 105 110 115 120

att ttt gca gtt ttg tta ttt ttt tcc tca ttg gaa act ccc aaa aat 1036  
 Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys Asn  
 125 130 135

ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct ttc 1084  
 Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe  
 140 145 150

ctt gac att tat ttt agt gga ctt tca gta act gaa aga tgg aaa ccc 1132  
 Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro  
 155 160 165

ttt ttg tac cgt gga aga att tgc aga aga ctt tca gtc gtt ttt gct 1180  
 Phe Leu Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala  
 170 175 180

gga atg att gag ctt aca ttt ttt att ctt tcc gca ttc aaa ctt aga 1228  
 Gly Met Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg  
 185 190 195 200

gac act cac ctc tgg tat ttt gta ata cct ggc ttt tcc att ttt gga 1276  
 Asp Thr His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly  
 205 210 215

att ttc tgg atg att tgt cat att att ttt ctt tta act ctt tgg gga 1324  
 Ile Phe Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly  
 220 225 230

ttc cat acc aaa tta aat gac tgc cat aaa gta tat ttt act cac agg 1372  
 278/735



345 350 355 360

atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag acc 1756  
Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr

365 370 375

tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg cat 1804  
Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His

380 385 390

tcc aaa cta aaa gct ttc ctc gaa ctt cgg aca gtg gat gga ccc aga 1852  
Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg

395 400 405

cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca gga 1900  
His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly

410 415 420

gag tgg gct cta gca ggt gga gat aca cta cgc ctt gac aca ctt ata 1948  
Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile

425 430 435 440

gaa tgg tgg aga gaa aag aat ggt tcc ttt tgt tcc cgg ctt att atc 1996  
Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile

445 450 455

gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg aaa 2044  
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460 465 470







<212> PRT

<213> Homo sapiens

<400> 81

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20 25 30

Ser Ile Ser Phe Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys

35 40 45

Phe Gly Arg Asn Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln

50 55 60

Val Ser Arg Val Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser

65 70 75 80

Ser Val Leu Ser Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu

85 90 95

Ile Val Asp Ser Arg Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro

100 105 110

Tyr Arg Cys Met Val Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys

115 120 125

Glu Asp Gly Glu Ser Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser



agagttcact gactccccag ccccaggtgg gccttgtgca catc atg acc agt ttt 296

Met Thr Ser Phe

1

gaa gat gct gac aca gaa gag aca gta act tgt ctc cag atg acg gtt 344

Glu Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu Gln Met Thr Val

5

10

15

20

tac cat cct ggc cag ttg cag tgt gga ata ttt cag tca ata agt ttt 392

Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln Ser Ile Ser Phe

25

30

35

aac aga gag aaa ctc cct tcc agc gaa gtg gtg aaa ttt ggc cga aat 440

Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys Phe Gly Arg Asn

40

45

50

tcc aac atc tgt cat tat act ttt cag gac aaa cag gtt tcc cga gtt 488

Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln Val Ser Arg Val

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60

65

cag ttt tct ctg cag ctg ttt aaa aaa ttc aac agc tca gtt ctc tcc 536

Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser Ser Val Leu Ser

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75

80

ttt gaa ata aaa aat atg agt aaa aag acc aat ctg atc gtg gac agc 584

Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu Ile Val Asp Ser

85

90

95

100







165

170

175

Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser

180

185

190

Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser

195

200

205

Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met

210

215

220

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr

225

230

235

240

Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser

245

250

255

Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu

260

265

270

Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr

275

280

285

Arg Phe Met Gly Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu

290

295

300

Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly

305

310

315

320





Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser  
1 5 10 15

cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc 214  
Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr  
20 25 30

cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc 262  
Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser  
35 40 45

ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac 310  
Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn  
50 55 60

tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt 358  
Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys  
65 70 75 80

gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc 406  
Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro  
85 90 95

cga aca gag gcg gca gag acc acc ccg atg tgg cag gcc ctg aag ctg 454  
Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu  
100 105 110



ctg aca gcc acc ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc 886  
Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser  
245 250 255

agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc 934  
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu  
260 265 270

ttc aca gtg ggc tca ctg cta gaa cag ggg gcc cta ctg gag gga acc 982  
Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr  
275 280 285

cgc ttc atg ggg cga cac agt gag ttt gct gcc cat gcc ctg cta ctc 1030  
 Arg Phe Met Gly Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu  
 290 295 300

tcc atc tgc tcc gca tgt ggc cag ctc ttc atc ttt tac acc att ggg 1078  
Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly  
305 310 315 320

cag ttt ggg gct gcc gtc ttc acc atc atc atg acc ctc cgc cag gcc 1126  
Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala  
325 330 335

ttt gcc atc ctt ctt tcc tgc ctt ctc tat ggc cac act gtc act gtg 1174  
Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val  
293/735

340

345

350

gtg gga ggg ctg ggg gtg gct gtg gtc ttt gct gcc ctc ctg ctc aga 1222  
Val Gly Gly Leu Gly Val Ala Val Val Phe Ala Ala Leu Leu Leu Arg

355

360

365

gtc tac gcg cgg ggc cgt cta aag caa cgg gga aag aag gct gtg cct 1270  
Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro

370

375

380

gtt gag tct cct gtg cag aag gtt tgagggtgga aagggcctga ggggtgaagt 1324  
Val Glu Ser Pro Val Gln Lys Val

385

390

gaaataggac cctcccacca tccccttctg ctgtaacctc tgaggagct ggctgaaagg 1384

gcaaaatgca ggtgttttct cagtatcaca gaccagctct gcagcagggg attggggagc 1444

ccaggaggca gccttccctt ttgccttaag tcacccatct tccagtaagc agttttattct 1504

gagccccggg ggtagacagt cctcagttag gggttttggg gagtttgggg tcaagagagc 1564

ataggtaggt tccacagtta ctcttccac aagttccctt aagtcttgcc ctagctgtgc 1624

tctgccacct tccagactca ctcccctctg caaataacct catttcttac cctggtgaga 1684

aaagcacaag cgggtgtaggc tccaatgctg ctttcccagg aggggtgaaga tgggtgctgtg 1744

ctgaggaaag gggatgcaga gccctgecca gcaccaccac ctccatgct cctggatccc 1804

taggctctgt tccatgagcc tgttgcaggt tttggtactt tagaaatgta acttttttgc 1864

cttataattt tattttatta aattaaatta ctgc 1898

- <210> 85
- <211> 432
- <212> PRT
- <213> Homo sapiens

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Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser  
35 40 45  
Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn  
50 55 60  
Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys  
65 70 75 80  
Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro  
85 90 95

Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu  
100 105 110

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val  
115 120 125

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser  
130 135 140

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg  
145 150 155 160

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln  
165 170 175

Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser  
180 185 190

Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser  
195 200 205

Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met  
210 215 220

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr  
225 230 235 240

Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser  
296/735



Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys  
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Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val  
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<210> 86

<211> 2018

<212> DNA

<213> Homo sapiens

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<222> (119).. (1414)

<400> 86

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atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc 166

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser

1 5 10 15

cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc 214

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr

20 25 30



cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc 262  
 Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser  
 35 40 45

ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac 310  
 Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn  
 50 55 60

tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt 358  
 Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys  
 65 70 75 80

gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc 406  
 Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro  
 85 90 95

cga aca gag gcg gca gag acc acc ccg atg tgg cag gcc ctg aag ctg 454  
 Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu  
 100 105 110

ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg act tgg ggt gtg 502  
 Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val  
 115 120 125

ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc aca gcc aca tea 550  
 Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser  
 130 135 140

ccg ggt gag cgc ttt acg gac tcg cag ttc ctg gtg cta atg aac cga 598  
 299/735

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg  
145 150 155 160

gtg ctg gca ctg att gtg gct ggc ctc tcc tgt gtt ctc tgc aag cag 646  
Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln  
165 170 175

ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt gcc agc ctg tcc 694  
Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser  
180 185 190

aat gtg ctt agc agc tgg tgc caa tac gaa gct ctt aag ttc gtc agc 742  
Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser  
195 200 205

ttc ccc acc cag gtg ctg gcc aag gcc tct aag gtg atc cct gtc atg 790  
Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met  
210 215 220

ctg atg gga aag ctt gtg tct cgg cgc agc tac gaa cac tgg gag tac 838  
Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr  
225 230 235 240

ctg aca gcc acc ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc 886  
Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser  
245 250 255

agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc 934  
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu

270

285

300

320

335

350

365

380

301/735

ctc tat ggc cac act gtc act gtg gtg gga ggg ctg ggg gtg gct gtg 1318  
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 385 390 395 400

gtc ttt gct gcc ctc ctg ctc aga gtc tac gcg cgg ggc cgt cta aag 1366  
 Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys  
 405 410 415

caa cgg gga aag aag gct gtg cct gtt gag tct cct gtg cag aag gtt 1414  
 Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val  
 420 425 430

tgagggtgga aagggcctga ggggtgaagt gaaataggac cctcccacca tccccttctg 1474

ctgtaacctc tgagggagct ggctgaaagg gcaaaatgca ggtgttttct cagtatcaca 1534

gaccagctct gcagcagggg attggggagc ccaggaggca gccttcctt ttgccttaag 1594

tcacccatct tccagtaage agttttattct gagccccggg ggtagacagt cctcagttag 1654

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aagttccctt aagtcttgcc ctagctgtgc tctgcccact tccagactca ctcccctctg 1774

caaatacctg catttcttac cctgggtgaga aaagcacaag cggtgtaggc tccaatgctg 1834

ctttcccagg aggggtgaaga tgggtgctgtg ctgaggaaag gggatgcaga gccctgccc 1894



85

90

95

Gln Asn Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe

100

105

110

Ala Glu Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala

115

120

125

Val Asn Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu

130

135

140

Arg Asp Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser

145

150

155

160

Val Asn Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu

165

170

175

Asn Asn Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile

180

185

190

Asn Ala Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg

195

200

205

Ile Phe Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu

210

215

220

Thr Arg Asn Met Val Gln Arg Gln Phe Ile Ala

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230

235

<210> 88

<211> 2717

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (111).. (815)

<400> 88

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aaatgctgag aaatacataa agttttcctc ttctgccttg gatatttata atg ggt 116

Met Gly

1

atc ggg aag tct aaa ata aat tcc tgc cct ctt tct ctc tct tgg ggt 164

Ile Gly Lys Ser Lys Ile Asn Ser Cys Pro Leu Ser Leu Ser Trp Gly

5

10

15

aaa agg cac agt gtg gat aca agt cca gga tat cat gag tca gat tcc 212

Lys Arg His Ser Val Asp Thr Ser Pro Gly Tyr His Glu Ser Asp Ser

20

25

30

aag aag tct gaa gat cta tcc ttg tgt aat gtt gct gag cac agc aat 260

Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His Ser Asn

35

40

45

50

aca aca gag ggg cca aca gga aag cag gag gga gct cag agc gtg gaa 308

Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser Val Glu

55

60

65

gag atg ttt gaa gaa gaa gct gaa gaa gag gtg ttc ctc aaa ttt gtg 356

Glu Met Phe Glu Glu Glu Ala Glu Glu Glu Val Phe Leu Lys Phe Val

70

75

80

ata ttg cat gca gaa gat gac aca gat gaa gcc ctc aga gtc cag aat 404

Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val Gln Asn

85

90

95

ctg cta caa gat gac ttt ggt atc aaa ccc gga ata atc ttt gct gag 452

Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe Ala Glu

100

105

110

atg cca tgt ggc aga cag cat tta cag aat tta gat gat gct gta aat 500

Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala Val Asn

115

120

125

130

ggg tct gca tgg aca atc tta tta ctg act gaa aac ttt tta aga gat 548

Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu Arg Asp

135

140

145

act tgg tgt aat ttc cag ttc tat acg tcc cta atg aac tcc gtt aac 596

Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser Val Asn

150

155

160

agg cag cat aaa tac aac tct gtt ata ccc atg cgg ccc ctg aac aat 644



Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu Asn Asn

165

170

175

ccc ctt ccc cga gaa agg act ccc ttt gcc ctc caa acc atc aat gcc 692

Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile Asn Ala

180

185

190

tta gag gaa gaa agt cgt gga ttt cct aca caa gta gaa aga att ttt 740

Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg Ile Phe

195

200

205

210

cag gag tct gtg tat aag aca caa caa act ata tgg aaa gag aca aga 788

Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu Thr Arg

215

220

225

aat atg gta caa aga caa ttt att gcc tgagatgaaa catataacat 835

Asn Met Val Gln Arg Gln Phe Ile Ala

230

235

gtggctggct cttgttttgt aaaccaaagt attaattctt acttgagaaa gcagtttcta 895

ggaaatgttt aaataaaaga gagtcttcac cttaaagaaa cctatggagc acaagaaaga 955

taaatttctg caggacagcc tataaaattg tgggtactttt tgatgtttca gtaaacttga 1015

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ggaatttctca atccatattc cttgtattga accttgaaca aaaacttgta tgacagacat 1135

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<211> 245

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Asp Trp Thr Asp Thr Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser

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Cys Cys Lys Leu Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val

180 185 190

Asn Asn Glu Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu

195 200 205

Met Gly Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu

210 215 220

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225 230 235 240

Gln Tyr Glu Ile Val

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<210> 90

<211> 1793

<212> DNA

<213> Homo sapiens

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ALL INFORMATION CONTAINED HEREIN IS UNCLASSIFIED  
DATE 01-21-2009 BY 60322 UCBAW/STP



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Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly

Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn

Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu

Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe

Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe

312/735

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Gln Tyr Glu Ile Val

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<211> 180

<212> PRT

<213> Homo sapiens

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45

Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg

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Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly

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75

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Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met

85

90

95

Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys

100

105

110

Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln

115

120

125

Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu

130

135

140

Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser

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Ala Leu Leu Gln

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Arg Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Leu Gly

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ata gga att ctg gtg ctc ctg atc atc gtg att ctg ggg gtg ccc ttg 148

Ile Gly Ile Leu Val Leu Leu Ile Ile Val Ile Leu Gly Val Pro Leu

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 Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu  
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 Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr  
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 155 160 165

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<213> Homo sapiens

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Glu Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu





<211> 2039

<212> DNA

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tcagtgactg gagagctcca aggaaagtct ctcagtgacc tggctgctgg cacc atg 177

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gac tca gaa aag aaa cgc ttt act gaa gag gcc acc aaa tac ttc cgg 225

Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr Phe Arg

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gag aga gtc agc cca gtg cat ctg caa atc ctg ctg act aac aat gaa 273

Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr Asn Asn Glu

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gcc tgg aag aga ttc gtg act gcg gct gaa ttg ccc agg gat gag gca 321

Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu Ala

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gat gct ctc tac gaa gct ctg aag aag ctt aga aca tat gca gct att 369  
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gag gac gaa tat gtg cag cag aaa gat gag cag ttt agg gaa tgg ttt 417  
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 70 75 80

ttg aaa gag ttt ccc caa gtc aag agg aag atc cag gag tcc ata gaa 465  
 Leu Lys Glu Phe Pro Gln Val Lys Arg Lys Ile Gln Glu Ser Ile Glu  
 85 90 95

aag ctt cgt gcc ctt gca aat ggt att gaa gag gtc cac aga ggc tgc 513  
 Lys Leu Arg Ala Leu Ala Asn Gly Ile Glu Glu Val His Arg Gly Cys  
 100 105 110

acc atc tcc aac gtg gtg tcc agc tcc act ggc gct gcc tct ggc atc 561  
 Thr Ile Ser Asn Val Val Ser Ser Ser Thr Gly Ala Ala Ser Gly Ile  
 115 120 125

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 Met Ser Leu Ala Gly Leu Val Leu Ala Pro Phe Thr Ala Gly Thr Ser  
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 323/735

Thr Gly Ile Thr Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ser Ala

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Glu Ala Glu Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu Lys

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Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser Leu

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gcc atc agg caa gcc aga gcc agg gcc cga ctc cct gtg acc acc tgg 897

Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr Trp

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cga atc tca gct gga agt ggt ggt caa gca gag aga acg att gca ggc 945

Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile Ala Gly

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acc acc cgg gca gtg agc aga gga gcc cgg atc ctg agt gcg acc act 993

Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr Thr

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Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr

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Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu

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Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly

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His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu

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Ile Cys Gly Ile Cys Ala Thr Arg Gly Glu His Thr Lys His Val Phe

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Cys Ser Ile Glu Asp Ala Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser

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Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg

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Leu Asp Thr Leu Glu Thr Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr

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Lys Asp Ser Asp Lys Val Lys Glu Phe Phe Glu Lys Leu Gln His Thr

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Leu Asp Gln Lys Lys Asn Glu Ile Leu Ser Asp Phe Glu Thr Met Lys  
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Leu Ala Val Met Gln Ala Tyr Asp Pro Glu Ile Asn Lys Leu Asn Thr  
 210 215 220

Ile Leu Gln Glu Gln Arg Met Ala Phe Asn Ile Ala Glu Ala Phe Lys  
 225 230 235 240

Asp Val Ser Glu Pro Ile Val Phe Leu Gln Gln Met Gln Glu Phe Arg  
 245 250 255

Glu Lys Ile Lys Val Ile Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu  
 260 265 270

Pro Ala Ser Pro Leu Met Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp  
 275 280 285

Ile Lys Leu Val Asp Val Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly  
 290 295 300

Thr Phe Ile Ser Lys Ile Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu  
 305 310 315 320

Ile Leu Leu Leu Gly Leu Val Ile Val Phe Gly Pro Thr Met Phe Leu  
 325 330 335

Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser  
 340 345 350  
 328/735

Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser  
 355 360 365

Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu  
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Arg Phe Lys Asn Phe Thr Leu Val Val Leu Asn Asn Val Ala Glu Phe  
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Val Cys Lys Tyr Lys Leu Leu  
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tttcccctgg gaaatagtaa ccctgccaaa tacatcagct tgtaggagac agaggatgtg 180

atg gag ctg ctt gaa gaa gat ctc aca tgc cct att tgt tgt agt ctg 228

Met Glu Leu Leu Glu Glu Asp Leu Thr Cys Pro Ile Cys Cys Ser Leu

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tgc tta gaa ggt atc tta gaa ggg agt gtg cgg aat tcc ttg tgg aga 324

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Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr

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Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly

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cac ttg ggg cag cct ctc aac att ttc tgc ctg act gat atg cag ctg 516

His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu

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Cys Ser Ile Glu Asp Ala Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser

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Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg

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Leu Asp Thr Leu Glu Thr Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr

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Lys Asp Ser Asp Lys Val Lys Glu Phe Phe Glu Lys Leu Gln His Thr

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ctg gat caa aag aag aat gaa att ctg tct gac ttt gag acc atg aaa 804

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245 250 255

gag aaa atc aaa gta atc aag gaa act cct tta cct ccc tct aat ttg 996  
Glu Lys Ile Lys Val Ile Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu  
260 265 270

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275 280 285

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332/735

340

345

350

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365

gtt ttt tac tgg gaa cag gtg aca gat ggg ttt ttc att ttc aat gaa 1332

Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu

370

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aga ttc aag aat ttt act ttg gtg gta ctg aac aat gtg gca gaa ttt 1380

Arg Phe Lys Asn Phe Thr Leu Val Val Leu Asn Asn Val Ala Glu Phe

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1409

Val Cys Lys Tyr Lys Leu Leu

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<210> 97

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<213> Homo sapiens

<400> 97

Met Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys

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Ser Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly

333/735



Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu  
180 185 190

Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr  
195 200 205

Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn  
210 215 220

Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser  
225 230 235 240

Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp  
245 250 255

Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr  
260 265 270

Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg  
275 280 285

Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu  
290 295 300

Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln  
305 310 315 320

Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val  
325 330 335

Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp  
 340 345 350

Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val  
 355 360 365

Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr  
 370 375 380

Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro  
 385 390 395 400

Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu  
 405 410 415

Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys  
 420 425 430

His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro  
 435 440 445

Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly  
 450 455 460

Asp  
 465



Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser  
5 10 15

atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac 575  
Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His  
20 25 30

agc tac tgc cac ttg tgt ata aca gac ttc ttt aaa aac cca agc caa 623  
Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln  
35 40 45

aag caa ctg agg cag gag aca ttc tgc tgt ccc cag tgt cgg gct cca 671  
Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro  
50 55 60 65

ttt cat atg gat agc ctc cga ccc aac aag cag ctg gga agc ctc att 719  
Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile  
70 75 80

gaa gcc ctc aaa gag acg gat caa gaa atg tca tgt gag gaa cac gga 767  
Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His Gly  
85 90 95

gag cag ttc cac ctg ttc tgc gaa gac gag ggg cag ctc atc tgc tgg 815  
Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys Trp  
100 105 110

cgc tgt gag cgg gca cca cag cac aaa ggg cac acc aca gct ctt gtt 863  
Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu Val  
338/735



115

120

125

gaa gac gta tgc cag ggc tac aag gaa aag ctc cag gaa gct gtg aca 911

Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Glu Ala Val Thr

130

135

140

145

aaa ctg aag caa ctt gaa gac aga tgt acg gag cag aag ctg tcc aca 959

Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser Thr

150

155

160

gca atg cga ata act aaa tgg aaa gag aag gta cag att cag aga caa 1007

Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg Gln

165

170

175

aaa atc cgg tct gac ttt aag aat ctc cag tgt ttc cta cat gag gaa 1055

Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu Glu

180

185

190

gag aag tct tat ctc tgg agg ctg gag aaa gaa gaa caa cag act ctg 1103

Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr Leu

195

200

205

agt aga ctg agg gac tat gag gct ggt ctg ggg ctg aag agc aat gaa 1151

Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn Glu

210

215

220

225

ctc aag agc cac atc ctg gaa ctg gag gaa aaa tgt cag ggc tca gcc 1199

Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser Ala

230

235

240

cag aaa ttg ctg cag aat gtg aat gac act ttg agc agg agt tgg gct 1247

Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp Ala

245

250

255

gtg aag ctg gaa aca tca gag gct gtc tcc ttg gaa ctt cat act atg 1295

Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr Met

260

265

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tgc aat gtt tcc aag ctt tac ttc gat gtg aag aaa atg tta agg agt 1343

Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg Ser

275

280

285

cat caa gtt agt gtg act ctg gat cca gat aca gct cat cac gaa cta 1391

His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu Leu

290

295

300

305

att ctc tct gag gat cgg aga caa gtg act cgt gga tac acc cag gag 1439

Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln Glu

310

315

320

aat cag gac aca tct tcc agg aga ttt act gcc ttc ccc tgt gtc ttg 1487

Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val Leu

325

330

335

ggc tgt gaa ggc ttc acc tca gga aga cgt tac ttt gaa gtg gat gtt 1535

Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val

340

345

350

ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag 1583

Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val Gln

355

360

365

agg ggc act ggc atg aag caa gag cct cag tct gga ttc tgg acc ctc 1631

Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr Leu

370

375

380

385

agg ctg tgc aaa aag aaa ggc tat gta gca ctt act tct ccc cca act 1679

Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr

390

395

400

tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg gac 1727

Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp

405

410

415

tat gag gcc gga gtt gta tcc ttt tat aac ggg aat act ggc tgc cac 1775

Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His

420

425

430

atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc cgg ccc tat 1823

Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr

435

440

445

ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac 1871

Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp

450

455

460

465

taaggaaaag agcagaagct ccttggttta accagcacag agaaaataat ataaatccca 1931

taaggggcag

1940

&lt;210&gt; 99

<211> 465

&lt;212&gt; PRT

<213> Homo sapiens

<400> 99

Met Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys  
1 5 10 15

Ser Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly  
20 25 30

His Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser  
35 40 45

Gln Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala  
50 55 60

Pro Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu  
65 70 75 80

Ile Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His  
85 90 95

Gly Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys  
342/735

100

105

110

Trp Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu

115

120

125

Val Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val

130

135

140

Thr Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser

145

150

155

160

Thr Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg

165

170

175

Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu

180

185

190

Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr

195

200

205

Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn

210

215

220

Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser

225

230

235

240

Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp

245

250

255

Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr  
260 265 270

Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg  
275 280 285

Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu  
290 295 300

Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln  
305 310 315 320

Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val  
325 330 335

Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp  
340 345 350

Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val  
355 360 365

Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr  
370 375 380

Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro  
385 390 395 400

Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu  
405 410 415

Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys  
 420 425 430

His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro  
 435 440 445

Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly  
 450 455 460

Asp  
 465

<210> 100  
 <211> 1940  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (477).. (1871)

<400> 100

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caccaaattct cagaagattc agaacttaga tgagtggggc ccaggacagg aaccctggag 120

ccttgaagg aggggagccc catctcccca gaagagcagt gacccagca gagaggggcc 180

tggtgtatca ctggaggaaa tagcctgcca aggaatacac gtcttcagaa gaagttctgt 240

gtggcttcaa gagactgata aaattgtgag aggaaaacag cctacccggt cctcttttct 300

tcaatacaaa atgagataat aggggttgga aggaaaacct tcaagaccta tggaagtcag 360

ttgcagccag ctcatcacat agaggtgcag gtgaggtgta ttttcatcac ggtggaaaat 420

tctggctgct tcattccat ctctagagcc aatattggag cttttcaata aaagct atg 479

Met

1

gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc 527

Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser

5

10

15

atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac 575

Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His

20

25

30

agc tac tgc cac ttg tgt ata aca gac ttc ttt aaa aac cca agc caa 623

Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln

35

40

45

aag caa ctg agg cag gag aca ttc tgc tgt ccc cag tgt cgg gct cca 671

Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro

50

55

60

65



ttt cat atg gat agc ctc cga ccc aac aag cag ctg gga agc ctc att 719

Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile

70

75

80

gaa gcc ctc aaa gag acg gat caa gaa atg tca tgt gag gaa cac gga 767

Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His Gly

85

90

95

gag cag ttc cac ctg ttc tgc gaa gac gag ggg cag ctc atc tgc tgg 815

Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys Trp

100

105

110

cgc tgt gag cgg gca cca cag cac aaa ggg cac acc aca gct ctt gtt 863

Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu Val

115

120

125

gaa gac gta tgc cag ggc tac aag gaa aag ctc cag aaa gct gtg aca 911

Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val Thr

130

135

140

145

aaa ctg aag caa ctt gaa gac aga tgt acg gag cag aag ctg tcc aca 959

Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser Thr

150

155

160

gca atg cga ata act aaa tgg aaa gag aag gta cag att cag aga caa 1007

Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg Gln

165

170

175

aaa atc cgg tct gac ttt aag aat ctc cag tgt ttc cta cat gag gaa 1055



290 295 300 305

att ctc tct gag gat cgg aga caa gtg act cgt gga tac acc cag gag 1439  
 Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln Glu  
 310 315 320

aat cag gac aca tct tcc agg aga ttt act gcc ttc ccc tgt gtc ttg 1487  
 Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val Leu  
 325 330 335

ggt tgt gaa ggc ttc acc tca gga aga cgt tac ttt gaa gtg gat gtt 1535  
 Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val  
 340 345 350

ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag 1583  
 Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val Gln  
 355 360 365

agg ggc act ggc atg aag caa gag cct cag tct gga ttc tgg acc ctc 1631  
 Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr Leu  
 370 375 380 385

agg ctg tgc aaa aag aaa ggc tat gta gca ctt act tct ccc cca act 1679  
 Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr  
 390 395 400

tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg gac 1727  
 Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp  
 405 410 415

tat gag gcc gga gtt gta tcc ttt tat aac ggg aat act ggc tgc cac 1775

Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His

420

425

430

atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc cgg ccc tat 1823

Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr

435

440

445

ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac 1871

Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp

450

455

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465

taaggaaaag agcagaagct ccttggttta accagcacag agaaaataat ataaatccca 1931

taagggcag

1940

<210> 101

<211> 685

<212> PRT

<213> Homo sapiens

<400> 101

Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser Thr Lys

1

5

10

15

Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser Lys Lys

20

25

30

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180

185

190

Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu Lys Leu

195

200

205

Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly Asp Phe

210

215

220

Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg Thr Ile

225

230

235

240

Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys Gln Gly

245

250

255

His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met Tyr Thr

260

265

270

Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys Glu Thr

275

280

285

Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser Leu Leu

290

295

300

Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn Pro Glu

305

310

315

320

Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe Leu Gln

325

330

335



Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr Ser Asn  
500 505 510

Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly Val Leu  
515 520 525

Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys Thr Val  
530 535 540

His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala Thr Asp  
545 550 555 560

Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr Phe Ser  
565 570 575

His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro Ser Val  
580 585 590

Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu Lys Ser  
595 600 605

Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln Val Asn  
610 615 620

Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn Glu Glu  
625 630 635 640

Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr Phe Arg  
354/735



645 650 655

Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys Asn Arg  
660 665 670

Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn  
675 680 685

<210> 102  
<211> 2783  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (128).. (2182)

<400> 102

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cggccggctc ggacgtgtga ccgcgcctag ggggtggcag cgggcagtgc ggggcggcaa 120

ggcgacc atg gag ctt ttg cgg act atc acc tac cag cca gcc gcc agc 169

Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser  
1 5 10

acc aaa atg tgc gag cag gcg ctg ggc aag ggt tgc gga gca gac tcg 217

Thr Lys Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser  
355/735

15

20

25

30

aag aag aag cgg ccg ccg cag ccc ccc gag gaa tcg cag cca cct cag 265

Lys Lys Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln

35

40

45

tcc cag gcg caa gtg ccc ccg gcg gcc cct cac cac cat cac cac cat 313

Ser Gln Ala Gln Val Pro Pro Ala Ala Pro His His His His His His

50

55

60

tcg cac tcg ggg ccg gag atc tcg cgg att atc gtc gac ccc acg act 361

Ser His Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr

65

70

75

ggg aag cgc tac tgc cgg gcc aaa gtg ctg gga aag ggt gcc ttt gca 409

Gly Lys Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala

80

85

90

aaa tgt tac gag atg aca gat ttg aca aat aac aaa gtc tac gcc gca 457

Lys Cys Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala

95

100

105

110

aaa att att cct cac agc aga gta gct aaa cct cat caa agg gaa aag 505

Lys Ile Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys

115

120

125

att gac aaa gaa ata gag ctt cac aga att ctt cat cat aag cat gta 553

Ile Asp Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val

130

135

140

gtg cag ttt tac cac tac ttc gag gac aaa gaa aac att tac att ctc 601

Val Gln Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu

145

150

155

ttg gaa tac tgc agt aga agg tca atg gct cat att ttg aaa gca aga 649

Leu Glu Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg

160

165

170

aag gtg ttg aca gag cca gaa gtt cga tac tac ctc agg cag att gtg 697

Lys Val Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val

175

180

185

190

tct gga ctg aaa tac ctt cat gaa caa gaa atc ttg cac aga gat ctc 745

Ser Gly Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu

195

200

205

aaa cta ggg aac ttt ttt att aat gaa gcc atg gaa cta aaa gtt ggg 793

Lys Leu Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly

210

215

220

gac ttc ggt ctg gca gcc agg cta gaa ccc ttg gaa cac aga agg aga 841

Asp Phe Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg

225

230

235

acg ata tgt ggt acc cca aat tat ctc tct cct gaa gtc ctc aac aaa 889

Thr Ile Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys

240

245

250

Gln Gly His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met  
255 260 265 270

tat aca atg tta cta ggg agg ccc cca ttt gaa act aca aat ctc aaa 985  
Tyr Thr Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys  
275 280 285

gaa act tat agg tgc ata agg gaa gca agg tat aca atg ccg tcc tca 1033  
Glu Thr Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser  
290 295 300

ttg ctg gct cct gcc aag cac tta att gct agt atg ttg tcc aaa aac 1081  
Leu Leu Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn  
305 310 315

cca gag gat cgt ccc agt ttg gat gac atc att cga cat gac ttt ttt 1129  
Pro Glu Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe  
320 325 330

ttg cag ggc ttc act ccg gac aga ctg tct tct agc tgt tgt cat aca 1177  
Leu Gln Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr  
335 340 345 350

gtt cca gat ttc cac tta tca agc cca gct aag aat ttc ttt aag aaa 1225  
Val Pro Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys  
355 360 365

gca gct gct gct ctt ttt ggt ggc aaa aaa gac aaa gca aga tat att 1273  
358/735

Ala Ala Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile  
 370 375 380

gac aca cat aat aga gtg tct aaa gaa gat gaa gac atc tac aag ctt 1321  
 Asp Thr His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu  
 385 390 395

agg cat gat ttg aaa aag act tca ata act cag caa ccc agc aaa cac 1369  
 Arg His Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His  
 400 405 410

agg aca gat gag gag ctc cag cca cct acc acc aca gtt gcc agg tct 1417  
 Arg Thr Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser  
 415 420 425 430

gga aca ccc gca gta gaa aac aag cag cag att ggg gat gct att cgg 1465  
 Gly Thr Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg  
 435 440 445

atg ata gtc aga ggg act ctt ggc agc tgt agc agc agc agt gaa tgc 1513  
 Met Ile Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys  
 450 455 460

ctt gaa gac agt acc atg gga agt gtt gca gac aca gtg gca agg gtt 1561  
 Leu Glu Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val  
 465 470 475

ctt cgg gga tgt ctg gaa aac atg ccg gaa gct gat tgc att ccc aaa 1609  
 Leu Arg Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys  
 359/735

480

485

490

gag cag ctg agc aca tca ttt cag tgg gtc acc aaa tgg gtt gat tac 1657

Glu Gln Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr

495

500

505

510

tct aac aaa tat ggc ttt ggg tac cag ctc tca gac cac acc gtc ggt 1705

Ser Asn Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly

515

520

525

gtc ctt ttc aac aat ggt gct cac atg agc ctc ctt cca gac aaa aaa 1753

Val Leu Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys

530

535

540

aca gtt cac tat tac gca gag ctt ggc caa tgc tca gtt ttc cca gca 1801

Thr Val His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala

545

550

555

aca gat gct cct gag caa ttt att agt caa gtg acg gtg ctg aaa tac 1849

Thr Asp Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr

560

565

570

ttt tct cat tac atg gag gag aac ctc atg gat ggt gga gat ctg cct 1897

Phe Ser His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro

575

580

585

590

agt gtt act gat att cga aga cct cgg ctc tac ctc ctt cag tgg cta 1945

Ser Val Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu

595

600

605

aaa tct gat aag gcc cta atg atg ctc ttt aat gat ggc acc ttt cag 1993

Lys Ser Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln

610

615

620

gtg aat ttc tac cat gat cat aca aaa atc atc atc tgt agc caa aat 2041

Val Asn Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn

625

630

635

gaa gaa tac ctt ctc acc tac atc aat gag gat agg ata tct aca act 2089

Glu Glu Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr

640

645

650

ttc agg ctg aca act ctg ctg atg tct ggc tgt tca tca gaa tta aaa 2137

Phe Arg Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys

655

660

665

670

aat cga atg gaa tat gcc ctg aac atg ctc tta caa aga tgt aac 2182

Asn Arg Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn

675

680

685

tgaaagactt ttcgaaatgga ccctatggga ctctctttt ccactgtgag atctacaggg 2242

aacccaaaag aatgatctag agtatgttga agaagatgga catgtggtgg tacgaaaaca 2302

attcccctgt ggcctgctgg actgggtgga accagaacag gctaaggcat acagttcttg 2362

actttggaca atccaagagt gaaccagaat gcagttttcc ttgagatacc tgttttaaaa 2422





Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr Thr Gln  
50 55 60

Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr Val Tyr  
65 70 75 80

Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met Cys Cys  
85 90 95

Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn Ala Gly  
100 105 110

Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly Cys Ile  
115 120 125

Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln Asp Val  
130 135 140

Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg  
145 150 155 160

Leu

<210> 104

<211> 1589

<212> DNA

&lt;221&gt; CDS

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5

10

Ser Ala Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn

15

20

25

30

Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly

35

40

45

Leu Val Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr

50

55

60

Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr

65

70

75

gtc tac gtg cag cac ccc atc acc ttt ttg gac cgc cct atc caa atg 351

Val Tyr Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met

80

85

90

tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac 399

Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn

95

100

105

110

gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg 447

Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly

115

120

125

tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag 495

Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln

130

135

140

gac gtg gac cat tac tgt ccc aac tgc aga gct ctc ctg ggc acc tac 543

Asp Val Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr

145

150

155

aag cgt ttg taggactcag ccagacgtgg agggagccgg gtgccgcagg 592

Lys Arg Leu

160

aagtcctttc cacctctcat ccagcttcac gcctgggtgga gggtctgccc tgggtggtctc 652

acctctccag ggggcccacc ttcatgtctt cttttggggg gaatacgtcg caaaactaac 712

aaatctccaa accccagaaa ttgctgcttg gagtcgtgca taggacttgc aaagacattc 772

cccttgagtg tcagttccac ggtttcctgc ctccctgaga ccctgagtec tgccatctaa 832

ctgtgatcat tgccctatec gaatatcttc ctgtgatctg ccatcagtgg ctcttttttc 892

ctgcttccat gggcctttct ggtggcagtc tcaaactgag aagccacagt tgccattattt 952

ttgaggctgt tctgcccaga gctcggctga accagccttt agtgcctacc attatcttat 1012

ccgtctcttc ccgtccctga tgacaaagat cttgccttac agactttaca ggcttggttt 1072

tgagattctg taactgcaga cttcattage acacagattc actttaattt ctttaattttt 1132

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tgccagatct tcagtgcgcc tttccataca gggatttttt tctcatagag taattatatg 1312

aacagttttt atgacctcct ttggtctga aatactttcg aacagaattt ctttttttta 1372

aaaaaaaaa gagatggggg cttactatgt tgcccaggct ggtgtcgaac tcctgggctc 1432

aagcgtcct tctgccttgg cctcccgaag tgctgggatt gcaggcataa gctaccatgc 1492

tgggcctgaa cataatttca agaggaggat ttataaaacc attttctgta atcaaattgat 1552

tggtgtcatt ttcccatttg ccaatgtagt ctcactt 1589



115

120

125

Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln Asp Val

130

135

140

Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg

145

150

155

160

Leu

<210> 106

<211> 1589

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70).. (552)

<400> 106

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ggcggtaaa atg tcg gtt cca gga cct tac cag gcg gcc act ggg cct tcc 111

Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser

1

5

10

tca gca cca tcc gca cct cca tcc tat gaa gag aca gtg gct gtt aac 159

Ser Ala Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn  
15 20 25 30

agt tat tac ccc aca cct cca gct ccc atg cct ggg cca act acg ggg 207  
Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly  
35 40 45

ctt gtg acg ggg cct gat ggg aag ggc atg aat cct cct tcg tat tat 255  
Leu Val Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr  
50 55 60

acc cag cca gcg ccc atc ccc aat aac aat cca att acc gtg cag acg 303  
Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr  
65 70 75

gtc tac gtg cag cac ccc atc acc ttt ttg gac cgc cct gtc caa atg 351  
Val Tyr Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Val Gln Met  
80 85 90

tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac 399  
Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn  
95 100 105 110

gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg 447  
Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly  
115 120 125

tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag 495  
Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln  
369/735



140

155

160

370/735





45

60

80

95

110

125

140

160

175

190

Asn Arg His Leu Arg Asp Glu Gly Leu Arg Leu Arg Lys Val Ala His

195

200

205

Ser Asp Lys Pro Gly Ser Thr Ser Thr Ala Ser Phe Arg Asp Asn Val

210

215

220

Thr Ser Pro Leu Pro Ser Leu Leu Val Val Ile Ala Ala Ile Phe Ile

225

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Gly Phe Phe Leu Gly Lys Phe Ile Leu

245

<210> 108

<211> 1595

<212> DNA

<213> Homo sapiens

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<222> (232).. (978)

<400> 108

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gaccagcgg gtggcccacc gaaccggtga cacagcggca ggcgttaggg ctcgggagcc 120

gcgagcctgg cctcgtccta gagctcggcc gagccgtcgc cgccgtcgtc ccccgccccc 180

agtcagcaaa ccgccgccgc gggcgcgccc ccgctctgcg ctgtctctcc g atg gcg 237

Met Ala

1

tcc gcc tca ggg gcc atg gcg aag cac gag cag atc ctg gtc ctc gat 285

Ser Ala Ser Gly Ala Met Ala Lys His Glu Gln Ile Leu Val Leu Asp

5

10

15

ccg ccc aca gac ctc aaa ttc aaa ggc ccc ttc aca gat gta gtc act 333

Pro Pro Thr Asp Leu Lys Phe Lys Gly Pro Phe Thr Asp Val Val Thr

20

25

30

aca aat ctt aaa ttg cga aat cca tcg gat aga aaa gtg tgt ttc aaa 381

Thr Asn Leu Lys Leu Arg Asn Pro Ser Asp Arg Lys Val Cys Phe Lys

35

40

45

50

gtg aag act aca gca cct cgc cgg tac tgt gtg agg ccc aac agt gga 429

Val Lys Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly

55

60

65

att att gac cca ggg tca act gtg act gtt tca gta atg cta cag ccc 477

Ile Ile Asp Pro Gly Ser Thr Val Thr Val Ser Val Met Leu Gln Pro

70

75

80

ttt gac tat gat ccg aat gaa aag agt aaa cac aag ttt atg gta cag 525

Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val Gln

85

90

95

aca att ttt gct cca cca aac act tca gat atg gaa gct gtg tgg aaa 573

374/735

Thr Ile Phe Ala Pro Pro Asn Thr Ser Asp Met Glu Ala Val Trp Lys  
 100 105 110

gag gca aaa cct gat gaa tta atg gat tcc aaa ttg aga tgc gta ttt 621  
 Glu Ala Lys Pro Asp Glu Leu Met Asp Ser Lys Leu Arg Cys Val Phe  
 115 120 125 130

gaa atg ccc aat gaa aat gat aaa ttg aat gat atg gaa cct agc aaa 669  
 Glu Met Pro Asn Glu Asn Asp Lys Leu Asn Asp Met Glu Pro Ser Lys  
 135 140 145

gct gtt cca ctg aat gca tct aag caa gat gga cct atg cca aaa cca 717  
 Ala Val Pro Leu Asn Ala Ser Lys Gln Asp Gly Pro Met Pro Lys Pro  
 150 155 160

cac agt gtt tca ctt aat gat acc gaa aca agg aaa cta atg gaa gag 765  
 His Ser Val Ser Leu Asn Asp Thr Glu Thr Arg Lys Leu Met Glu Glu  
 165 170 175

tgt aaa aga ctt cag gga gaa atg atg aag cta tca gaa gaa aat cgg 813  
 Cys Lys Arg Leu Gln Gly Glu Met Met Lys Leu Ser Glu Glu Asn Arg  
 180 185 190

cac ctg aga gat gaa ggt tta agg ctc aga aag gta gca cat tcg gat 861  
 His Leu Arg Asp Glu Gly Leu Arg Leu Arg Lys Val Ala His Ser Asp  
 195 200 205 210

aaa cct gga tca acc tca act gca tcc ttc aga gat aat gtc acc agt 909  
 Lys Pro Gly Ser Thr Ser Thr Ala Ser Phe Arg Asp Asn Val Thr Ser  
 375/735

215

220

225

cct ctt cct tca ctt ctt gtt gta att gca gcc att ttc att gga ttc 957  
Pro Leu Pro Ser Leu Leu Val Val Ile Ala Ala Ile Phe Ile Gly Phe

230

235

240

ttt cta ggg aaa ttc atc ttg tagagtgaag catgcagagt gctgtttcct 1008  
Phe Leu Gly Lys Phe Ile Leu

245

tttttttttt tctcttgacc agaaaaagat ttgtttacct accatttcat tggtagtatg 1068

gcccacggtg accatttttt tgtgtgtaca gcgtcatata ggctttgcct ttaatgatct 1128

cttacgggta gaaaacacaa taaaaacaaa ctgttcggct actggacagg ttgtatatta 1188

ccagatcatt actagcagat gtcagttgca cattgagtc tttatgaaat tcataaataa 1248

agaattgttc tttctttgtg gttttaataa gagttcaaga attgttcaga gtcttgtaaa 1308

tggtatttta ataatccctt taaattttat ctgttgctgt tacctcttga aatatgattt 1368

atttagattg ctaatccac tcattcagga aatgccaaga ggtattcctt ggggaaatgg 1428

tgcctcttac agtgtaaatt tttcctcctt tacctttgct aatatcatgg cagaattttt 1488

cttatccctt gtgaggcagt tgttgactga gtttttcatt cttacaatcc tgtcccatgg 1548

tatttaacat aaaaaaaaaat aaaactgtta acagattcctt gctcgat 1595

<210> 109

<211> 540

<212> PRT

<213> Homo sapiens

<400> 109

Met Gly Thr Thr Ala Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val

1 5 10 15

Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln

20 25 30

Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser

35 40 45

Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln

50 55 60

His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser

65 70 75 80

Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu

85 90 95

Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro

100 105 110

Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu  
 115 120 125

Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser  
 130 135 140

Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp  
 145 150 155 160

Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn  
 165 170 175

Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro  
 180 185 190

Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu  
 195 200 205

Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg  
 210 215 220

Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala  
 225 230 235 240

Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His  
 245 250 255

Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu  
 260 265 270



Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln  
275 280 285

Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro  
290 295 300

Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser  
305 310 315 320

Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu  
325 330 335

Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly  
340 345 350

Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys  
355 360 365

Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys  
370 375 380

Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala  
385 390 395 400

Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg  
405 410 415

Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu  
379/735

420

425

430

Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg

435

440

445

Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu

450

455

460

Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp

465

470

475

480

Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val

485

490

495

Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly

500

505

510

Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly

515

520

525

Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu

530

535

540

<210> 110

<211> 1810

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (102).. (1721)

<400> 110

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gaggacccac ctctgagtgt ccagtgggtca gttgccccag g atg ggg acc aca gcc 116

Met Gly Thr Thr Ala

1

5

aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct 164

Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser

10

15

20

gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac 212

Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His

25

30

35

ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga 260

Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg

40

45

50

agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt 308

Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe

55

60

65

gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct 356

Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro

70

75

80

85

ctc caa cag gaa aag ctg cta cct gcc caa ctc cct gct gaa aag gaa 404  
Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu Pro Ala Glu Lys Glu

90

95

100

gtg ggt ccc cct ctc cct cag gaa gct gtc ccc ctc caa aaa gag ctg 452  
Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro Leu Gln Lys Glu Leu

105

110

115

ccc tct ctc cag cac ccc aat gaa cag aag gaa gga acg cca gct cca 500  
Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu Gly Thr Pro Ala Pro

120

125

130

ttt ggg gac cag agc cat cca gaa cct gag tcc tgg aat gca gcc cag 548  
Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser Trp Asn Ala Ala Gln

135

140

145

cac tgc caa cag gac cgg tcc caa ggg ggc tgg ggc cac cgg ctg gat 596  
His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp Gly His Arg Leu Asp

150

155

160

165

ggc ttc ccc cct ggg cgg cct tct cca gac aat ctg aac caa atc tgc 644  
Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn Leu Asn Gln Ile Cys

170

175

180

ctt cct aac cgt cag cat gtg gta tat ggt ccc tgg aac cta cca cag 692  
Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro Trp Asn Leu Pro Gln

185

190

195

tcc agc tac tcc cac ctc act cgc cag ggt gag acc ctc aat ttc ctg 740  
 Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu Thr Leu Asn Phe Leu  
 200 205 210

gag att gga tat tcc cgc tgc tgc cac tgc cgc agc cac aca aac cgc 788  
 Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg  
 215 220 225

cta gag tgt gcc aaa ctt gtg tgg gag gaa gca atg agc cga ttc tgt 836  
 Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala Met Ser Arg Phe Cys  
 230 235 240 245

gag gcc gag ttc tcg gtc aag acc cga ccc cac tgg tgc tgc acg cgg 884  
 Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr Arg  
 250 255 260

cag ggg gag gct cgg ttc tcc tgc ttc cag gag gaa gct ccc cag cca 932  
 Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu Glu Ala Pro Gln Pro  
 265 270 275

cac tac cag ctc cgg gcc tgc ccc agc cat cag cct gat att tcc tcg 980  
 His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln Pro Asp Ile Ser Ser  
 280 285 290

ggt ctt gag ctg cct ttc cct cct ggg gtg ccc aca ttg gac aat atc 1028  
 Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro Thr Leu Asp Asn Ile  
 295 300 305

aag aac atc tgc cac ctg agg cgc ttc cgc tct gtg cca cgc aac ctg 1076  
 Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu  
 310 315 320 325

cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg 1124  
 Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu Ala Leu Ile Gln Leu  
 330 335 340

gag agg gag ttc cag cgc tgc tgc cgc cag ggg aac aat cac acc tgt 1172  
 Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys  
 345 350 355

aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag 1220  
 Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys Tyr Cys Asp Arg Glu  
 360 365 370

tat gct gtg aag acc cac cac cac ttg tgt tgc cgc cac cct ccc agc 1268  
 Tyr Ala Val Lys Thr His His His Leu Cys Cys Arg His Pro Pro Ser  
 375 380 385

cct act cgg gat gag tgc ttt gcc cgt cgg gct cct tac ccc aac tat 1316  
 Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala Pro Tyr Pro Asn Tyr  
 390 395 400 405

gac cgg gac atc ttg acc att gac atc ggt cga gtc acc ccc aac ctc 1364  
 Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg Val Thr Pro Asn Leu  
 410 415 420

atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat 1412  
 384/735

Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His  
 425 430 435

att cct ggg ctg atc cac aac atg act gcc cgc tgc tgt gac ctg cca 1460  
 Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro  
 440 445 450

ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc 1508  
 Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile  
 455 460 465

aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc ctc 1556  
 Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu  
 470 475 480 485

tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc 1604  
 Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val Asn Cys Phe Asn Ile  
 490 495 500

aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc 1652  
 Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala  
 505 510 515

aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc 1700  
 Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser  
 520 525 530

acc tct gag ccc aag gaa gaa tgagtcaccc cagagcccta gagggtcaga 1751  
 Thr Ser Glu Pro Lys Glu Glu

535

540

tggggggaac cccaccctgc cccacccatc tgaacactca ttacactaaa cacctcttg 1810

<210> 111

<211> 540

<212> PRT

<213> Homo sapiens

<400> 111

Met Gly Thr Thr Ala Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val  
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Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln  
20 25 30

Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser  
35 40 45

Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln  
50 55 60

His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser  
65 70 75 80

Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu  
85 90 95



Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro  
 100 105 110

Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu  
 115 120 125

Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser  
 130 135 140

Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp  
 145 150 155 160

Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn  
 165 170 175

Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro  
 180 185 190

Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu  
 195 200 205

Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg  
 210 215 220

Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala  
 225 230 235 240

Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His  
 245 250 255



405

410

415

Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu

420

425

430

Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg

435

440

445

Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu

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455

460

Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp

465

470

475

480

Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val

485

490

495

Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly

500

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Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly

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Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu

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<210> 112

<211> 1810

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (102).. (1721)

<400> 112

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gaggacccac ctctgagtgt ccagtgggtca gttgccccag g atg ggg acc aca gcc 116  
Met Gly Thr Thr Ala  
1 5

aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct 164  
Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser  
10 15 20

gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac 212  
Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His  
25 30 35

ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga 260  
Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg  
40 45 50

agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt 308  
Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe  
55 60 65



ctt cct aac cgt cag cat gtg gta tat ggt ccc tgg aac cta cca cag 692

Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro Trp Asn Leu Pro Gln

185

190

195

tcc agc tac tcc cac ctc act cgc cag ggt gag acc ctc aat ttc ctg 740

Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu Thr Leu Asn Phe Leu

200

205

210

gag att gga tat tcc cgc tgc tgc cac tgc cgc agc cac aca aac cgc 788

Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg

215

220

225

cta gag tgt gcc aaa ctt gtg tgg gag gaa gca atg agc cga ttc tgt 836

Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala Met Ser Arg Phe Cys

230

235

240

245

gag gcc gag ttc tcg gtc aag acc cga ccc cac tgg tgc tgc acg cgg 884

Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr Arg

250

255

260

cag ggg gag gct cgg ttc tcc tgc ttc cag gag gaa gct ccc cag cca 932

Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu Glu Ala Pro Gln Pro

265

270

275

cac tac cag ctc cgg gcc tgc ccc agc cat cag cct gat att tcc tcg 980

His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln Pro Asp Ile Ser Ser

280

285

290

ggt ctt gag ctg cct ttc cct cct ggg gtg ccc aca ttg gac aat atc 1028

Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro Thr Leu Asp Asn Ile  
 295 300 305

aag aac atc tgc cac ctg agg cgc ttc cgc tct gtg cca cgc aac ctg 1076  
 Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu  
 310 315 320 325

cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg 1124  
 Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu Ala Leu Ile Gln Leu  
 330 335 340

gag agg gag ttc cag cgc tgc tgc cgc cag ggg aac aat cac acc tgt 1172  
 Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys  
 345 350 355

aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag 1220  
 Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys Tyr Cys Asp Arg Glu  
 360 365 370

tat gct gtg aag acc cac cac cac ttg tgt tgc cgc cac cct ccc agc 1268  
 Tyr Ala Val Lys Thr His His His Leu Cys Cys Arg His Pro Pro Ser  
 375 380 385

cct act cgg gat gag tgc ttt gcc cgt cgg gct cct tac ccc aac tat 1316  
 Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala Pro Tyr Pro Asn Tyr  
 390 395 400 405

gac cgg gac atc ttg acc att gac atc agt cga gtc acc ccc aac ctc 1364  
 Asp Arg Asp Ile Leu Thr Ile Asp Ile Ser Arg Val Thr Pro Asn Leu  
 393/735

410

415

420

atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat 1412

Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His

425

430

435

att cct ggg ctg atc cac aac atg act gcc cgc tgc tgt gac ctg cca 1460

Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro

440

445

450

ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc 1508

Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile

455

460

465

aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc ctc 1556

Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu

470

475

480

485

tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc 1604

Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val Asn Cys Phe Asn Ile

490

495

500

aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc 1652

Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala

505

510

515

aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc 1700

Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser

520

525

530







Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro  
245 250 255

Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser  
260 265 270

Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu  
275 280 285

Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln  
290 295 300

Ala Ser Glu Gln Thr Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met  
305 310 315 320

Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp  
325 330 335

Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu  
340 345 350

Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser  
355 360 365

Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile  
370 375 380





Ile Gln Trp Tyr Ile Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys  
160 165 170  
175 180 185

aaa aga gat ccc tgc cca cat cag gtg gac tgt ttc ctc tct cgc ccc 809  
Lys Arg Asp Pro Cys Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro  
190 195 200

acg gag aaa acc atc ttc atc atc ttc atg ctg gtg gtg tcc ttg gtg 857  
Thr Glu Lys Thr Ile Phe Ile Ile Phe Met Leu Val Val Ser Leu Val  
205 210 215

tcc ctg gcc ttg aat atc att gaa ctc ttc tat gtt ttc ttc aag ggc 905  
Ser Leu Ala Leu Asn Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly  
220 225 230 235

gtt aag gat cgg gtt aag gga aag agc gac cct tac cat gcg acc agt 953  
Val Lys Asp Arg Val Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser  
240 245 250

ggt gcg ctg agc cct gcc aaa gac tgt ggg tct caa aaa tat gct tat 1001  
Gly Ala Leu Ser Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr  
255 260 265

ttc aat ggc tgc tcc tca cca acc gct ccc ctc tcg cct atg tct cct 1049  
Phe Asn Gly Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro  
270 275 280











Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys  
 130 135 140

Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu  
 145 150 155 160

Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile  
 165 170 175

Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys  
 180 185 190

Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile  
 195 200 205

Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn  
 210 215 220

Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val  
 225 230 235 240

Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro  
 245 250 255

Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser  
 260 265 270

Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu  
 275 280 285

Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln  
 290 295 300

Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met  
 305 310 315 320

Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp  
 325 330 335

Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu  
 340 345 350

Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser  
 355 360 365

Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile  
 370 375 380

<210> 116

<211> 3074

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

$\langle 222 \rangle \quad (201) \dots (1346)$ 

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aacagcagcg gagttttaaa ctttaaatag acaggtctga gtgcctgaac ttgccttttc 120

attttacttc atcctccaag gagttcaatc acttggcgtg acttcactac ttttaagcaa 180

aagagtgggtg cccaggcaac atg ggt gac tgg agc gcc tta ggc aaa ctc ctt 233

Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu

1

5

10

gac aag gtt caa gcc tac tca act gct gga ggg aag gtg tgg ctg tca 281

Asp Lys Val Gln Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser

15

20

25

gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt gag tca 329

Val Leu Phe Ile Phe Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser

30

35

40

gcc tgg gga gat gag cag tct gcc ttt cgt tgt aac act cag caa cct 377

Ala Trp Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro

45

50

55

ggt tgt gaa aat gtc tgc tat gac aag tct ttc cca atc tct cat gtg 425

Gly Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val

60

65

70

75





300 305 310 315

gaa caa aat cga atg ggg cag gcg gga agc acc atc tct aac tcc cat 1193  
Glu Gln Asn Arg Met Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His

320 325 330

gca cag cct ttt gat ttc ccc gat gat aac cag aat tct aaa aaa cta 1241  
Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu  
335 340 345

gct gct gga cat gaa tta cag cca cta gcc att gtg gac cag cga cct 1289  
Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro  
350 355 360

tca agc aga gcc agc agt cgt gcc agc agc aga cct cgg cct gat gac 1337  
Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp  
365 370 375

ctg gag atc tagatacagg cttgaaagca tcaagattcc actcaattgt 1386  
Leu Glu Ile  
380

ggagaagaaa aaaggtgctg tagaaagtgc accaggtggt aattttgatc cgggtggaggt 1446

ggtactcaac agccttattc atgaggctta gaaaacacaa agacattaga atacctaggt 1506

tcaactggggg tgtatggggt agatgggtgg agagggaggg gataagagag gtgcatgttg 1566

gtatttaaag tagtggatc aaagaactta gattataaat aagagttcca ttaggtgata 1626



catagataag ggctttttct ccccgcaaac acccctaaga atggttctgt gtatgtgaat 1686

gagcgggtgg taattgtggc taaatatttt tgttttacca agaaactgaa ataattctgg 1746

ccaggaataa atacttcctg aacatcttag gtcttttcaa caagaaaaag acagaggatt 1806

gtccttaagt ccctgctaaa acattccatt gttaaaattt gcactttgaa ggtaagcttt 1866

ctaggcctga ccctccaggt gtcaatggac ttgtgctact atattttttt attcttggtg 1926

tcagtttaaa attcagacaa ggcccacaga ataagatttt ccatgcattt gcaaatacgt 1986

atattctttt tccatccact tgcacaatat cattaccatc actttttcat cattcctcag 2046

ctactactca cattcattta atggtttctg taaacatttt taagacagtt gggatgtcac 2106

ttaacatttt ttttttgagc taaagtcagg gaatcaagcc atgcttaata tttacaatc 2166

acttatatgt gtgtcgaaga gtttgttttg tttgtcatgt attggtacaa gcagatacag 2226

tataaactca caaacacaga tttgaaaata atgcacatat ggtgttcaaa tttgaacctt 2286

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gcaagtaaag cacacttttt ttttctccta aaatgttttt ccctgtgtat cctattatgg 2406

atactggttt tgtaattat gattctttat tttctctcct ttttttagga tatagcagta 2466

atgctattac tgaaatgaat ttcctttttc tgaaatgtaa tcattgatgc ttgaatgata 2526

gaatttttagt actgtaaaca ggcttttagtc attaatgtga gagacttaga aaaaaatgct 2586

tagagtggac tattaaatgt gcctaaatga attttgcagt aactgggtatt cttgggtttt 2646

cctacttaat acacagtaat tcagaacttg tattctatta tgagtttagc agtcttttgg 2706

agtgaccagc aactttgatg tttgcactaa gattttatatt ggaatgcaag agaggttgaa 2766

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cagtttctcc aaatgccttt tttaaaactc atcacagaag attggtgaaa atgctgagta 2886

tgacactttt cttcttgcac gcatgtcagc tacataaaca gttttgtaca atgaaaatta 2946

ctaatttggt tgacattcca tgttaaacta cggtcatggt cagcttcatt gcatgtaatg 3006

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tttagtat 3074

<210> 117

<211> 398

<212> PRT

<213> Homo sapiens

<400> 117

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu Cys Ile Trp Met  
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Ser Ala Leu Phe Leu Gly Val Gly Val Arg Ala Glu Glu Ala Gly Ala  
20 25 30

Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln  
35 40 45

Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser  
50 55 60

Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser  
65 70 75 80

Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu Ala Trp Asn Gly  
85 90 95

Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala Asp Glu Leu Arg  
100 105 110

Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met Lys Asp Lys Asn  
115 120 125

Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe Leu Lys Glu Phe  
130 135 140

Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg Arg Leu Arg Ala  
145 150 155 160

Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr Thr Ile Ala Asn

165

170

175

Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile Leu Thr Leu Val

180

185

190

Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser Leu Val Leu Leu

195

200

205

Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu Thr Gly Ile Thr

210

215

220

Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr Gln Ala Gln Ala

225

230

235

240

His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys Glu Val Lys Glu

245

250

255

Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu Ala Gly Asn Thr

260

265

270

Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg Ala Leu Arg Arg

275

280

285

Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser Ala Ser Arg Pro

290

295

300

Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu Gln Val Glu Arg

305                      310                      315                      320

Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly Val Lys Leu Thr

325                      330                      335

Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr Leu

340                      345                      350

Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr Ala

355                      360                      365

Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu Lys Leu Asn Ile

370                      375                      380

Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu

385                      390                      395

<210> 118

<211> 2054

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76).. (1269)

<400> 118

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aggccctgca ggcac atg gag gga gct gct ttg ctg aga gtc tct gtc ctc 111

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu

1

5

10

tgc atc tgg atg agt gca ctt ttc ctt ggt gtg gga gtg agg gca gag 159

Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Gly Val Arg Ala Glu

15

20

25

gaa gct gga gcg agg gtg caa caa aac gtt cca agt ggg aca gat act 207

Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr

30

35

40

gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg 255

Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met

45

50

55

60

gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag 303

Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys

65

70

75

gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag 351

Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu

80

85

90

gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc agg aat gag gca 399

Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala

95

100

105



Thr Gly Ile Thr Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr  
 225 230 235

caa gcc caa gcc cac gac ctg gtc atc aaa agc ctt gac aaa ttg aag 831  
 Gln Ala Gln Ala His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys  
 240 245 250

gag gtg aag gag ttt ttg ggt gag aac ata tcc aac ttt ctt tcc tta 879  
 Glu Val Lys Glu Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu  
 255 260 265

gct ggc aat act tac caa ctc aca cga ggc att ggg aag gac atc cgt 927  
 Ala Gly Asn Thr Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg  
 270 275 280

gcc ctc aga cga gcc aga gcc aat ctt cag tca gta ccg cat gcc tca 975  
 Ala Leu Arg Arg Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser  
 285 290 295 300

gcc tca cgc ccc cgg gtc act gag cca atc tca gct gaa agc ggt gaa 1023  
 Ala Ser Arg Pro Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu  
 305 310 315

cag gtg gag aga gtt aat gaa ccc agc atc ctg gaa atg agc aga gga 1071  
 Gln Val Glu Arg Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly  
 320 325 330

gtc aag ctc acg gat gtg gcc cct gta agc ttc ttt ctt gtg ctg gat 1119  
 Val Lys Leu Thr Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp



335 340 345  
gta gtc tac ctc gtg tac gaa tca aag cac tta cat gag ggg gca aag 1167  
Val Val Tyr Leu Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys  
350 355 360

tca gag aca gct gag gag ctg aag aag gtg gct cag gag ctg gag gag 1215  
Ser Glu Thr Ala Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu  
365 370 375 380

aag cta aac att ctc aac aat aat tat aag att ctg cag gcg gac caa 1263  
Lys Leu Asn Ile Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln  
385 390 395

gaa ctg tgaccacagg gcagggcagc caccaggaga gatatgcctg gcaggggcca 1319  
Glu Leu

ggacaaaatg caaacttttt ttttttctga gacagagtct tgctctgtcg ccaagttgca 1379

gtgagccgag atategccac tgcactccag cctgggtgac agagcgagac tccatctcaa 1439

aaaaaaaaa aaaaagaata tattgacgga agaatagaga ggaggcttga aggaaccagc 1499

aatgagaagg ccaggaaaag aaagagctga aaatggagaa agcccaagag ttagaacagt 1559

tggatacagg agaagaaaca gcggtccac tacagacca gccccaggtt caatgtcctc 1619

cgaagaatga agtctttccc tggatgatgt cccctgccct gtctttccag catccactct 1679

ggtggttgtc atgtgatggg tccccctccag gttactaaag ggtgcatgtc ccctgcttga 1799

acactgaagg gcaggtgggtg agccatggcc atgggtcccca gctgaggagc aggtgtccct 1859

gagaacccaa acttcccaga gagtatgtga gaaccaacca atgaaaacag tcccatcgct 1919

cttaccoggt aagtaaacag tcagaaaatt agcatgaaag cagtttagca ttgggaggaa 1979

gtcagatct ctagagctgt cttgtccccg cccaggattg acctgtgtaa gtcccaataa 2039

actcacctac tcate 2054

actcacctac tcate

2054

<210> 119

<211> 398

<212> PRT

<213> Homo sapiens

<400> 119

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu Cys Ile Trp Met

1

5

10

15

Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu Glu Ala Gly Ala

20

25

30

Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln

35

40

45







gaa gct gga gcg agg gtg caa caa aac gtt cca agt ggg aca gat act 207  
 Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr  
 30 35 40

gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg 255  
 Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met  
 45 50 55 60

gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag 303  
 Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys  
 65 70 75

gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag 351  
 Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu  
 80 85 90

gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc agg aat gag gca 399  
 Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala  
 95 100 105

gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg 447  
 Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met  
 110 115 120

aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt 495  
 Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe  
 125 130 135 140



Glu Val Lys Glu Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu  
 255 260 265

gct ggc aat act tac caa ctc aca cga ggc att ggg aag gac atc cgt 927  
 Ala Gly Asn Thr Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg  
 270 275 280

gcc ctc aga cga gcc aga gcc aat ctt cag tca gta ccg cat gcc tca 975  
 Ala Leu Arg Arg Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser  
 285 290 295 300

gcc tca cgc ccc cgg gtc act gag cca atc tca gct gaa agc ggt gaa 1023  
 Ala Ser Arg Pro Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu  
 305 310 315

cag gtg gag aga gtt aat gaa ccc agc atc ctg gaa atg agc aga gga 1071  
 Gln Val Glu Arg Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly  
 320 325 330

gtc aag ctc acg gat gtg gcc cct gta agc ttc ttt ctt gtg ctg gat 1119  
 Val Lys Leu Thr Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp  
 335 340 345

gta gtc tac ctc gtg tac gaa tca aag cac tta cat gag ggg gca aag 1167  
 Val Val Tyr Leu Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys  
 350 355 360

tca gag aca gct gag gag ctg aag aag gtg gct cag gag ctg gag gag 1215  
 Ser Glu Thr Ala Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu  
 426/735



380

395



85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu  
100 105

<210> 122  
<211> 1546  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (89).. (412)

<400> 122  
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gcccgcgccgc tcagcgtccg ccgccgcc atg gga gtg cag gtg gaa acc atc 112  
Met Gly Val Gln Val Glu Thr Ile  
1 5

tcc cca gga gac ggg cgc acc ttc ccc aag cgc ggc cag acc tgc gtg 160  
Ser Pro Gly Asp Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val  
10 15 20

gtg cac tac acc ggg atg ctt gaa gat gga aag aaa ttt gat tcc tcc 208  
Val His Tyr Thr Gly Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser  
25 30 35 40

cgg gac aga aac aag ccc ttt aag ttt atg cta ggc aag cag gag gtg 256

Arg Asp Arg Asn Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val

45

50

55

atc cga ggc tgg gaa gaa ggg gtt gcc cag atg agt gtg ggt cag aga 304

Ile Arg Gly Trp Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg

60

65

70

gcc aaa ctg act ata tct cca gat tat gcc tat ggt gcc act ggg cac 352

Ala Lys Leu Thr Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His

75

80

85

cca ggc atc atc cca cca cat gcc act ctc gtc ttc gat gtg gag ctt 400

Pro Gly Ile Ile Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu

90

95

100

cta aaa ctg gaa tgacaggaat ggcctcctcc cttagctccc tggtcttgga 452

Leu Lys Leu Glu

105

tctgccatgg agggatctgg tgcctccaga catgtgcaca tgaatccata tggagctttt 512

cctgatgttc cactccactt tgtatagaca tctgccctga ctgaatgtgt tctgtcactc 572

agctttgctt ccgacacctc tgtttctct tcccctttct cctcgatatgt gtgtttacct 632

aaactatatg ccataaacct caagttactc attttatattt gttttcattt tgggggtgaag 692

attcagtttc agtcttttgg atataggttt ccaattaagt acatggtcaa gtattaacag 752

cacaagtggg aggttaacat tagaatagga attggtgttg gggggggggg ttgcaagaat 812

atatttatttt aatttttttg atgaaatttt tatctattat atattaaaca ttcttgctgc 872

tgcgctgcaa agccatagca gatttgaggg gctgttgagg actgaattac tctccaagtt 932

gagagatgtc ttgggttaa attaaaagcc ctacctaaaa ctgaggtggg gatggggaga 992

gcctttgcct ccaccattcc caccaccct ccccttaaac cctctgcctt tgaaagtaga 1052

tcatgttcac tgcaatgctg gacctacag gtatctgtcc ctgggccagc agggacctct 1112

gaagccttct ttgtggcctt tttttttttt tcatcctgtg gtttttctaa tggactttca 1172

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attgacagtt tcaattgaag gtgctgtttg tagacttaac acccagtgaa agcccagcca 1292

tcatgacaaa tccttgaatg ttctcttaag aaaatgatgc tggtcacgc agcttcagca 1352

tctcctgttt ttgatgctt ggctccctct gctgactca gtttctggc ttttctccc 1412

tcagccctt ctcaccctt tgctgtcctg tgtagtgatt tggtgagaaa tcgttgctgc 1472

acccttcccc cagcaccatt tatgagtctc aagttttatt attgcaataa aagtgttta 1532

tgccggcttt tctc

1546



Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu Lys Leu Pro Ile Ser  
115 120 125

Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly Phe Ser Leu Val Ala  
130 135 140

Lys Gly Gln Glu Gly Val Lys Trp Ser Glu Leu Ile Lys Ile Val Met  
145 150 155 160

Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile Met Ser Gly Ile Leu  
165 170 175

Phe Phe Leu Val Arg Ala Phe Ile Leu His Lys Ala Asp Pro Val Pro  
180 185 190

Asn Gly Leu Arg Ala Leu Pro Val Phe Tyr Ala Cys Thr Val Gly Ile  
195 200 205

Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro Leu Leu Gly Phe Asp  
210 215 220

Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser Val Gly Cys Ala Val  
225 230 235 240

Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys Pro Arg Met Lys Arg  
245 250 255

Lys Ile Glu Arg Glu Ile Lys Cys Ser Pro Ser Glu Ser Pro Leu Met  
260 265 270

Glu Lys Lys Asn Ser Leu Lys Glu Asp His Glu Glu Thr Lys Leu Ser

275

280

285

Val Gly Asp Ile Glu Asn Lys His Pro Val Ser Glu Val Gly Pro Ala

290

295

300

Thr Val Pro Leu Gln Ala Val Val Glu Glu Arg Thr Val Ser Phe Lys

305

310

315

320

Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu Arg Leu Pro Ser Val

325

330

335

Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr Val Asn Gly Ala Val

340

345

350

Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser Gln Ala Val Ser Asn

355

360

365

Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His Thr Val His Lys Asp

370

375

380

Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu His Leu Ala Lys Val

385

390

395

400

Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro Leu Arg Arg Asn Asn

405

410

415

Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly Met Pro Leu Asp Ser

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430

445

460

480

495

510

525

540

560

575

Trp Val Trp Gly Arg Arg Val Ile Gln Thr Met Gly Lys Asp Leu Thr  
580 585 590

Pro Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu Leu Ala Ser Ala Leu  
595 600 605

Thr Val Val Ile Ala Ser Asn Ile Gly Leu Pro Ile Ser Thr Thr His  
610 615 620

Cys Lys Val Gly Ser Val Val Ser Val Gly Trp Leu Arg Ser Lys Lys  
625 630 635 640

Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe Met Ala Trp Phe Val  
645 650 655

Thr Val Pro Ile Ser Gly Val Ile Ser Ala Ala Ile Met Ala Ile Phe  
660 665 670

Arg Tyr Val Ile Leu Arg Met  
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<210> 124

<211> 2916

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

ALL INFORMATION CONTAINED HEREIN IS UNCLASSIFIED  
DATE 06-03-2003 BY 60322 UCBAW



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65



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85







agg ctt ccc agc gtg gac ttg aaa gag gaa acc agc ata gat agc acc 1121  
 Arg Leu Pro Ser Val Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr  
 335 340 345

gtg aat ggt gca gtg cag ttg cct aat ggg aac ctt gtc cag ttc agt 1169  
 Val Asn Gly Ala Val Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser  
 350 355 360

caa gcc gtc agc aac caa ata aac tcc agt ggc cac tac cag tat cac 1217  
 Gln Ala Val Ser Asn Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His  
 365 370 375

acc gtg cat aag gat tcc ggc ctg tac aaa gag cta ctc cat aaa tta 1265  
 Thr Val His Lys Asp Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu  
 380 385 390 395

cat ctt gcc aag gtg gga gat tgc atg gga gac tcc ggt gac aaa ccc 1313  
 His Leu Ala Lys Val Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro  
 400 405 410

tta agg cgc aat aat agc tat act tcc tat acc atg gca ata tgt ggc 1361  
 Leu Arg Arg Asn Asn Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly  
 415 420 425

atg cct ctg gat tca ttc cgt gcc aaa gaa ggt gaa cag aag ggc gaa 1409  
 Met Pro Leu Asp Ser Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Glu  
 430 435 440

gaa atg gag aag ctg aca tgg cct aat gca gac tcc aag aag cga att 1457  
 Glu Met Glu Lys Leu Thr Trp Pro Asn Ala Asp Ser Lys Lys Arg Ile  
 445 450 455

cga atg gac agt tac acc agt tac tgc aat gct gtg tct gac ctt cac 1505  
 Arg Met Asp Ser Tyr Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His  
 460 465 470 475

tca gca tct gag ata gac atg agt gtc aag gca gag atg ggt cta ggt 1553  
 Ser Ala Ser Glu Ile Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly  
 480 485 490

gac aga aaa gga agt aat ggc tct cta gaa gaa tgg tat gac cag gat 1601  
 Asp Arg Lys Gly Ser Asn Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp  
 495 500 505

aag cct gaa gtc tct ctc ctc ttc cag ttc ctg cag atc ctt aca gcc 1649  
 Lys Pro Glu Val Ser Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala  
 510 515 520

tgc ttt ggg tca ttc gcc cat ggt ggc aat gac gta agc aat gcc att 1697  
 Cys Phe Gly Ser Phe Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile  
 525 530 535

ggg cct ctg gtt gct tta tat ttg gtt tat gac aca gga gat gtt tct 1745  
 Gly Pro Leu Val Ala Leu Tyr Leu Val Tyr Asp Thr Gly Asp Val Ser  
 540 545 550 555





Ile Met Ala Ile Phe Arg Tyr Val Ile Leu Arg Met

670

675

tgagattaaa atttgtgtca atgtttggga ccatcttagg tattcctgct cccctgaaga 2187

atgattacag tgtaaacaga agactgacaa gagtcttttt atttgggagc cagaggaggg 2247

aagtgttact tgtgtataa ctgcttttgt gctaaatatg aattgtctca aaattagctg 2307

tgtaaaatag cccgggttcc actggctcct gctgaggtec cctttccttc tgggctgtga 2367

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acagagcatg ctctgcgttg ttggtttcac cagcttctgc cctcacatgc acagggattt 2547

aacaacaaaa atataactac aacttccctt gtagtctctt atataagtag agtccttggt 2607

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gatgaggttc tttgaacaca gtgaaaattt aaattagtaa cttttttgca agcagtttat 2727

tgactgttat tgctaagaag aagtaagaaa gaaaaagcct gttggcaatc ttggttattt 2787

ctttaagatt tctggcagtg tgggatggat gaatgaagtg gaatgtgaac tttgggcaag 2847

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agtttttag

2916

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<211> 288

<212> PRT

<213> Homo sapiens

<400> 125

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Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln Ala Glu Asn Ala Glu

20

25

30

Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr Arg Asp Gly Phe Lys

35

40

45

Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val Ala Leu Glu Glu Glu

50

55

60

Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala Pro Val Tyr Phe Pro

65

70

75

80

Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln Asp Leu Ala Phe Trp

85

90

95

Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr Thr Pro Ala Met Gln

100

105

110

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Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg Thr Glu Pro Glu Leu

115

120

125

Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly Asp Leu Ser Gly Gly

130

135

140

Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu Asp Leu Pro Ser Ser

145

150

155

160

Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn Ile Ala Ser Ala Thr

165

170

175

Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn Ser Leu Glu Met Thr

180

185

190

Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala Lys Thr Ala Phe Leu

195

200

205

Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu Leu Leu Thr His Asp

210

215

220

Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly Leu Arg Gln Arg Ala

225

230

235

240

Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu Thr Pro Arg Gly Lys

245

250

255

Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu Leu Arg Trp Val Leu

445/735

260 265 270

Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val Gly Leu Tyr Ala Met  
275 280 285

<210> 126  
<211> 1550  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (81).. (944)

<400> 126

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acgagcccag caccggccgg atg gag cgt ccg caa ccc gac agc atg ccc cag 113

Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln

1 5 10

gat ttg tca gag gcc ctg aag gag gcc acc aag gag gtg cac acc cag 161

Asp Leu Ser Glu Ala Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln

15 20 25

gca gag aat gct gag ttc atg agg aac ttt cag aag ggc cag gtg acc 209

Ala Glu Asn Ala Glu Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr

30 35 40



gac ctg ccc agc tct ggc gag ggc ctg gcc ttc ttc acc ttc ccc aac 593

Asp Leu Pro Ser Ser Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn

160

165

170

att gcc agt gcc acc aag ttc aag cag ctc tac cgc tcc cgc atg aac 641

Ile Ala Ser Ala Thr Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn

175

180

185

tcc ctg gag atg act ccc gca gtc agg cag agg gtg ata gaa gag gcc 689

Ser Leu Glu Met Thr Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala

190

195

200

aag act gcg ttc ctg ctc aac atc cag ctc ttt gag gag ttg cag gag 737

Lys Thr Ala Phe Leu Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu

205

210

215

ctg ctg acc cat gac acc aag gac cag agc ccc tca cgg gca cca ggg 785

Leu Leu Thr His Asp Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly

220

225

230

235

ctt cgc cag cgg gcc agc aac aaa gtg caa gat tct gcc ccc gtg gag 833

Leu Arg Gln Arg Ala Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu

240

245

250

act ccc aga ggg aag ccc cca ctc aac acc cgc tcc cag gct ccg ctt 881

Thr Pro Arg Gly Lys Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu

255

260

265

ctc cga tgg gtc ctt aca ctc agc ttt ctg gtg gcg aca gtt gct gta 929

Leu Arg Trp Val Leu Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val  
270 275 280

ggg ctt tat gcc atg tgaatgcagg catgctggct cccagggcca tgaactttgt 984  
Gly Leu Tyr Ala Met  
285

ccggtggaag gccttctttc tagagaggga attctcttgg ctggttccct taccgtgggc 1044  
actgaaggct ttcagggcct ccagccctct cactgtgtcc ctctctctgg aaaggaggaa 1104  
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tcaaatagcag tattttttgtt gtgttctgtt gtttttatag cagggttggg gtggtttttg 1464  
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tgtgaaataa taaacaacat tgtctg 1550

<211> 135

<212> PRT

<213> Homo sapiens

<400> 127

Met Ala Cys Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu

1 5 10 15

Cys Leu Arg Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val

20 25 30

Leu Asn Leu Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro

35 40 45

Arg Phe Asn Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys

50 55 60

Asp Gly Gly Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe

65 70 75 80

Gln Pro Gly Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn

85 90 95

Leu Thr Val Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg

100 105 110

Leu Asn Leu Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys

115 120 125



Ile Lys Cys Val Ala Phe Asp

130 135

<210> 128

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50).. (454)

<400> 128

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Met Ala Cys

1

ggt ctg gtc gcc agc aac ctg aat ctc aaa cct gga gag tgc ctt cga 106

Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu Cys Leu Arg

5 10 15

gtg cga ggc gag gtg gct cct gac gct aag agc ttc gtg ctg aac ctg 154

Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val Leu Asn Leu

20 25 30 35

ggc aaa gac agc aac aac ctg tgc ctg cac ttc aac cct cgc ttc aac 202

Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro Arg Phe Asn

40 45 50



1. 2. 3. 4. 5. 6. 7. 8. 9. 10. 11. 12. 13. 14. 15. 16. 17. 18. 19. 20. 21. 22. 23. 24. 25. 26. 27. 28. 29. 30. 31. 32. 33. 34. 35. 36. 37. 38. 39. 40. 41. 42. 43. 44. 45. 46. 47. 48. 49. 50. 51. 52. 53. 54. 55. 56. 57. 58. 59. 60. 61. 62. 63. 64. 65. 66. 67. 68. 69. 70. 71. 72. 73. 74. 75. 76. 77. 78. 79. 80. 81. 82. 83. 84. 85. 86. 87. 88. 89. 90. 91. 92. 93. 94. 95. 96. 97. 98. 99. 100. 101. 102. 103. 104. 105. 106. 107. 108. 109. 110. 111. 112. 113. 114. 115. 116. 117. 118. 119. 120. 121. 122. 123. 124. 125. 126. 127. 128. 129. 130. 131. 132. 133. 134. 135. 136. 137. 138. 139. 140. 141. 142. 143. 144. 145. 146. 147. 148. 149. 150. 151. 152. 153. 154. 155. 156. 157. 158. 159. 160. 161. 162. 163. 164. 165. 166. 167. 168. 169. 170. 171. 172. 173. 174. 175. 176. 177. 178. 179. 180. 181. 182. 183. 184. 185. 186. 187. 188. 189. 190. 191. 192. 193. 194. 195. 196. 197. 198. 199. 200. 201. 202. 203. 204. 205. 206. 207. 208. 209. 210. 211. 212. 213. 214. 215. 216. 217. 218. 219. 220. 221. 222. 223. 224. 225. 226. 227. 228. 229. 230. 231. 232. 233. 234. 235. 236. 237. 238. 239. 240. 241. 242. 243. 244. 245. 246. 247. 248. 249. 250. 251. 252. 253. 254. 255. 256. 257. 258. 259. 260. 261. 262. 263. 264. 265. 266. 267. 268. 269. 270. 271. 272. 273. 274. 275. 276. 277. 278. 279. 280. 281. 282. 283. 284. 285. 286. 287. 288. 289. 290. 291. 292. 293. 294. 295. 296. 297. 298. 299. 300. 301. 302. 303. 304. 305. 306. 307. 308. 309. 310. 311. 312. 313. 314. 315. 316. 317. 318. 319. 320. 321. 322. 323. 324. 325. 326. 327. 328. 329. 330. 331. 332. 333. 334. 335. 336. 337. 338. 339. 340. 341. 342. 343. 344. 345. 346. 347. 348. 349. 350. 351. 352. 353. 354. 355. 356. 357. 358. 359. 360. 361. 362. 363. 364. 365. 366. 367. 368. 369. 370. 371. 372. 373. 374. 375. 376. 377. 378. 379. 380. 381. 382. 383. 384. 385. 386. 387. 388. 389. 390. 391. 392. 393. 394. 395. 396. 397. 398. 399. 400. 401. 402. 403. 404. 405. 406. 407. 408. 409. 410. 411. 412. 413. 414. 415. 416. 417. 418. 419. 420. 421. 422. 423. 424. 425. 426. 427. 428. 429. 430. 431. 432. 433. 434. 435. 436. 437. 438. 439. 440. 441. 442. 443. 444. 445. 446. 447. 448. 449. 450. 451. 452. 453. 454. 455. 456. 457. 458. 459. 460. 461. 462. 463. 464. 465. 466. 467. 468. 469. 470. 471. 472. 473. 474. 475. 476. 477. 478. 479. 480. 481. 482. 483. 484. 485. 486. 487. 488. 489. 490. 491. 492. 493. 494. 495. 496. 497. 498. 499. 500. 501. 502. 503. 504. 505. 506. 507. 508. 509. 510. 511. 512. 513. 514. 515. 516. 517. 518. 519. 520. 521. 522. 523. 524. 525. 526. 527. 528. 529. 530. 531. 532. 533. 534. 535. 536. 537. 538. 539. 540. 541. 542. 543. 544. 545. 546. 547. 548. 549. 550. 551. 552. 553. 554. 555. 556. 557. 558. 559. 560. 561. 562. 563. 564. 565. 566. 567. 568. 569. 570. 571. 572. 573. 574. 575. 576. 577. 578. 579. 580. 581. 582. 583. 584. 585. 586. 587. 588. 589. 590. 591. 592. 593. 594. 595. 596. 597. 598. 599. 600. 601. 602. 603. 604. 605. 606. 607. 608. 609. 610. 611. 612. 613. 614. 615. 616. 617. 618. 619. 620. 621. 622. 623. 624. 625. 626. 627. 628. 629. 630. 631. 632. 633. 634. 635. 636. 637. 638. 639. 640. 641. 642. 643. 644. 645. 646. 647. 648. 649. 650. 651. 652. 653. 654. 655. 656. 657. 658. 659. 660. 661. 662. 663. 664. 665. 666. 667. 668. 669. 670. 671. 672. 673. 674. 675. 676. 677. 678. 679. 680. 681. 682. 683. 684. 685. 686. 687. 688. 689. 690. 691. 692. 693. 694. 695. 696. 697. 698. 699. 700. 701. 702. 703. 704. 705. 706. 707. 708. 709. 710. 711. 712. 713. 714. 715. 716. 717. 718. 719. 720. 721. 722. 723. 724. 725. 726. 727. 728. 729. 730. 731. 732. 733. 734. 735. 736. 737. 738. 739. 740. 741. 742. 743. 744. 745. 746. 747. 748. 749. 750. 751. 752. 753. 754. 755. 756. 757. 758. 759. 760. 761. 762. 763. 764. 765. 766. 767. 768. 769. 770. 771. 772. 773. 774. 775. 776. 777. 778. 779. 780. 781. 782. 783. 784. 785. 786. 787. 788. 789. 790. 791. 792. 793. 794. 795. 796. 797. 798. 799. 800. 801. 802. 803. 804. 805. 806. 807. 808. 809. 810. 811. 812. 813. 814. 815. 816. 817. 818. 819. 820. 821. 822. 823. 824. 825. 826. 827. 828. 829. 830. 831. 832. 833. 834. 835. 836. 837. 838. 839. 840.

10

1                      5                      10                      15

20 25 30

35                      40                      45

50                      55                      60

65                      70                      75                      80

85                      90                      95

100                      105                      110

115                  120                  125

His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile

130

135

140

Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu

145

150

155

160

Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro

165

170

175

Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg

180

185

190

Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr

195

200

205

Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu Asp Leu

210

215

220

Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Leu

225

230

235

240

Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly Tyr Glu

245

250

255

Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn Pro Tyr

260

265

270

Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu Met Gln

275

280

285

Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys Arg Lys  
 290 295 300

Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val  
 305 310 315 320

Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala  
 325 330 335

Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe  
 340 345 350

Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu Leu Asp  
 355 360 365

Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly Lys Gln  
 370 375 380

Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp  
 385 390 395 400

Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu  
 405 410 415

Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu Lys Phe  
 420 425 430

Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe Ser Asn  
 455/735





Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu

1 5 10

ctt att ttt aat gca gtg cat gta aaa gat gca ggc ttt tat gtc tgt 157

Leu Ile Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys

15 20 25

cga gtt aat aac aat ttc acc ttt gaa ttc agc cag tgg tca cag ctg 205

Arg Val Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu

30 35 40

gat gtt tgc gac atc cca gag agc ttc cag aga agt gtt gat ggc gtc 253

Asp Val Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val

45 50 55 60

tct gaa tcc aag ttg caa atc tgt gtt gaa cca act tcc caa aag ctg 301

Ser Glu Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu

65 70 75

atg cca ggc agc aca ttg gtt tta cag tgt gtt gct gtt gga agc cct 349

Met Pro Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro

80 85 90

att cct cac tac cag tgg ttc aaa aat gaa tta cca tta aca cat gag 397

Ile Pro His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu

95 100 105

acc aaa aag cta tac atg gtg cct tat gtg gat ttg gaa cac caa gga 445

Thr Lys Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly



110

115

120

acc tac tgg tgt cat gta tat aat gat cga gac agt caa gat agc aag 493

Thr Tyr Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys

125

130

135

140

aag gta gaa atc atc ata gga aga aca gat gag gca gtg gag tgc act 541

Lys Val Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr

145

150

155

gaa gat gaa tta aat aat ctt ggt cat cct gat aat aaa gag caa aca 589

Glu Asp Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr

160

165

170

act gac cag cct ttg gcg aag gac aag gtt gcc ctt ttg ata gga aat 637

Thr Asp Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn

175

180

185

atg aat tac cgg gag cac ccc aag ctc aaa gct cct ttg gtg gat gtg 685

Met Asn Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val

190

195

200

tac gaa ttg act aac tta ctg aga cag ctg gac ttc aaa gtg gtt tca 733

Tyr Glu Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser

205

210

215

220

ctg ttg gat ctt act gaa tat gag atg cgt aat gct gtg gat gag ttt 781

Leu Leu Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe

225

230

235

tta ctc ctt tta gac aag gga gta tat ggg tta tta tat tat gca gga 829

Leu Leu Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly

240

245

250

cat ggt tat gaa aat ttt ggg aac agc ttc atg gtc ccc gtt gat gct 877

His Gly Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala

255

260

265

cca aat cca tat agg tct gaa aat tgt ctg tgt gta caa aat ata ctg 925

Pro Asn Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu

270

275

280

aaa ttg atg caa gaa aaa gaa act gga ctt aat gtg ttc tta ttg gat 973

Lys Leu Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp

285

290

295

300

atg tgt agg aaa aga aat gac tac gat gat acc att cca atc ttg gat 1021

Met Cys Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp

305

310

315

gca cta aaa gtc acc gcc aat att gtg ttt gga tat gcc acg tgt caa 1069

Ala Leu Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln

320

325

330

gga gca gaa gct ttt gaa atc cag cat tct gga ttg gca aat gga atc 1117

Gly Ala Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile

335

340

345

ttt atg aaa ttt tta aaa gac aga tta tta gaa gat aag aaa atc act 1165

Phe Met Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr

350

355

360

gtg tta ctg gat gaa gtt gca gaa gat atg ggt aag tgt cac ctt acc 1213

Val Leu Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr

365

370

375

380

aaa ggc aaa cag gct cta gag att cga agt agt tta tct gag aag aga 1261

Lys Gly Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg

385

390

395

gca ctt act gat cca ata cag gga aca gaa tat tct gct gaa tct ctt 1309

Ala Leu Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu

400

405

410

gtg cgg aat cta cag tgg gcc aag gct cat gaa ctt cca gaa agt atg 1357

Val Arg Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met

415

420

425

tgt ctt aag ttt gac tgt ggt gtt cag att caa tta gga ttt gca gct 1405

Cys Leu Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala

430

435

440

gag ttt tcc aat gtc atg atc atc tat aca agt ata gtt tac aaa cca 1453

Glu Phe Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro

445

450

455

460

ccg gag ata ata atg tgt gat gcc tac gtt act gat ttt cca ctt gat 1501

Pro Glu Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp

465

470

475

cta gat att gat cca aaa gat gca aat aaa ggc aca cct gaa gaa act 1549

Leu Asp Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr

480

485

490

ggc agc tac ttg gta tca aag gat ctt ccc aag cat tgc ctc tat acc 1597

Gly Ser Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr

495

500

505

aga ctc agt tca ctg caa aaa tta aag gaa cat cta gtc ttc aca gta 1645

Arg Leu Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val

510

515

520

tgt tta tca tat cag tac tca gga ttg gaa gat act gta gag gac aag 1693

Cys Leu Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys

525

530

535

540

cag gaa gtg aat gtt ggg aaa cct ctc att gct aaa tta gac atg cat 1741

Gln Glu Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His

545

550

555

cga ggt ttg gga agg aag act tgc ttt caa act tgt ctt atg tct aat 1789

Arg Gly Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn

560

565

570

ggt cct tac cag agt tct gca gcc acc tca gga gga gca ggg cat tat 1837

Gly Pro Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr

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575

580

585

cac tca ttg caa gac cca ttc cat ggt gtt tac cat tca cat cct ggt 1885

His Ser Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly

590

595

600

aat cca agt aat gtt aca cca gca gat agc tgt cat tgc agc cgg act 1933

Asn Pro Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr

605

610

615

620

cca gat gca ttt att tca agt ttc gct cac cat gct tca tgt cat ttt 1981

Pro Asp Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe

625

630

635

agt aga agt aat gtg cca gta gag aca act gat gaa ata cca ttt agt 2029

Ser Arg Ser Asn Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser

640

645

650

ttc tct gac agg ctc aga att tct gaa aaa tgacctcctt gtttttgaaa 2079

Phe Ser Asp Arg Leu Arg Ile Ser Glu Lys

655

660

gtagcataa ttttagatgc ctgtgaaata gtactgcact tacataaagt gagacattgt 2139

gaaaaggcaa atttgtatat gtagagaaag aatagtagta actgtttcat agcaaacttc 2199

aggactttga gatgttgaaa ttacattatt taattacaga ctctctcttt ct 2251

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DATE 06-08-2001 BY 60322 UCBAW



&lt;400&gt; 131

1                      5                      10                      15

20 25 30

35                      40                      45

50                      55                      60

65                      70                      75                      80

85                      90                      95

100                      105                      110

115                      120                      125

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Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu  
435 440 445

Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys  
450 455 460

Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu  
465 470 475 480

Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala  
485 490 495

Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met  
500 505 510

Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu  
515 520 525

Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly  
530 535 540

Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu  
545 550 555 560

Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg  
565 570 575

Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu  
580 585 590

Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe

595

600

605

Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu

610

615

620

Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp

625

630

635

640

Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser

645

650

655

Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu

660

665

670

Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu

675

680

685

Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu

690

695

700

Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly

705

710

715

720

Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro

725

730

735

Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser

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750

765

780

800

815

820

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gcccctgcct ccgcggctcg gaggcgagcg gaaggtgccc cggggcccag gcccgtagc 120

gggcggggcgg gagccccggc agtccggggt cgccggcgag ggcc atg tcg ctg ttg 176

Met Ser Leu Leu

1

ggg gac ccg cta cag gcc ctg ccg ccc tcg gcc gcc ccc acg ggg ccg 224

Gly Asp Pro Leu Gln Ala Leu Pro Pro Ser Ala Ala Pro Thr Gly Pro

5 10 15 20

ctg ctc gcc cct ccg gcc ggc gcg acc ctc aac cgc ctg cgg gag ccg 272

Leu Leu Ala Pro Pro Ala Gly Ala Thr Leu Asn Arg Leu Arg Glu Pro

25 30 35

ctg ctg cgg agg ctc agc gag ctc ctg gat cag gcg ccc gag ggc cgg 320

Leu Leu Arg Arg Leu Ser Glu Leu Leu Asp Gln Ala Pro Glu Gly Arg

40 45 50

ggc tgg agg aga ctg gcg gag ctg gcg ggg agt cgc ggg cgc ctc cgc 368

Gly Trp Arg Arg Leu Ala Glu Leu Ala Gly Ser Arg Gly Arg Leu Arg

55 60 65

ctc agt tgc cta gac ctg gag cag tgt tct ctt aag gta ctg gag cct 416

Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys Val Leu Glu Pro

70 75 80

gaa gga agc ccc agc ctg tgt ctg ctg aag tta atg ggt gaa aaa ggt 464

Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met Gly Glu Lys Gly

|   |     |     |     |     |
|---|-----|-----|-----|-----|
| 85  | 90  | 95  | 100 |     |
| tgc aca gtc aca gaa ttg agt gat ttc ctg cag gct atg gaa cac act |     |     |     | 512 |
| Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala Met Glu His Thr |     |     |     |     |
|   | 105 | 110 | 115 |     |
| gaa gtt ctt cag ctt ctc agc ccc cca gga ata aag att act gta aac |     |     |     | 560 |
| Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys Ile Thr Val Asn |     |     |     |     |
|   | 120 | 125 | 130 |     |
| cca gag tca aag gca gtc ttg gct gga cag ttt gtg aaa ctg tgt tgc |     |     |     | 608 |
| Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val Lys Leu Cys Cys |     |     |     |     |
|   | 135 | 140 | 145 |     |
| cgg gca act gga cat cct ttt gtt caa tat cag tgg ttc aaa atg aat |     |     |     | 656 |
| Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp Phe Lys Met Asn |     |     |     |     |
|   | 150 | 155 | 160 |     |
| aaa gag att cca aat gga aat aca tca gag ctt att ttt aat gca gtg |     |     |     | 704 |
| Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile Phe Asn Ala Val |     |     |     |     |
|   | 165 | 170 | 175 | 180 |
| cat gta aaa gat gca ggc ttt tat gtc tgt cga gtt aat aac aat ttc |     |     |     | 752 |
| His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val Asn Asn Asn Phe |     |     |     |     |
|   | 185 | 190 | 195 |     |
| acc ttt gaa ttc agc cag tgg tca cag ctg gat gtt tgc gac atc cca |     |     |     | 800 |
| Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp Ile Pro |     |     |     |     |
|   | 200 | 205 | 210 |     |

gag agc ttc cag aga agt gtt gat ggc gtc tct gaa tcc aag ttg caa 848

Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys Leu Gln

215

220

225

atc tgt gtt gaa cca act tcc caa aag ctg atg cca ggc agc aca ttg 896

Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser Thr Leu

230

235

240

gtt tta cag tgt gtt gct gtt gga agc cct att cct cac tac cag tgg 944

Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr Gln Trp

245

250

255

260

ttc aaa aat gaa tta cca tta aca cat gag acc aaa aag cta tac atg 992

Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu Tyr Met

265

270

275

gtg cct tat gtg gat ttg gaa cac caa gga acc tac tgg tgt cat gta 1040

Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys His Val

280

285

290

tat aat gat cga gac agt caa gat agc aag aag gta gaa atc atc ata 1088

Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile Ile Ile

295

300

305

gga aga aca gat gag gca gtg gag tgc act gaa gat gaa tta aat aat 1136

Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu Asn Asn

310

315

320















180

185

190

Thr Pro Cys Ser Lys Val Thr Ala Pro Gln Pro Ala Ala Thr Asn Gly

195

200

205

Asp Leu Ala Ser Arg Ser Asn Ile Ala Phe Met Gly Thr Leu Val Arg

210

215

220

Cys Gly Lys Ala Lys Gly Val Val Ile Gly Thr Gly Glu Asn Ser Glu

225

230

235

240

Phe Gly Glu Val Phe Lys Met Met Gln Ala Glu Glu Ala Pro Lys Thr

245

250

255

Pro Leu Gln Lys Ser Met Asp Leu Leu Gly Lys Gln Leu Ser Phe Tyr

260

265

270

Ser Phe Gly Ile Ile Gly Ile Ile Met Leu Val Gly Trp Leu Leu Gly

275

280

285

Lys Asp Ile Leu Glu Met Phe Thr Ile Ser Val Ser Leu Ala Val Ala

290

295

300

Ala Ile Pro Glu Gly Leu Pro Ile Val Val Thr Val Thr Leu Ala Leu

305

310

315

320

Gly Val Met Arg Met Val Lys Lys Arg Ala Ile Val Lys Lys Leu Pro

325

330

335

Ile Val Glu Thr Leu Gly Cys Cys Asn Val Ile Cys Ser Asp Lys Thr  
340 345 350

Gly Thr Leu Thr Lys Asn Glu Met Thr Val Thr His Ile Phe Thr Ser  
355 360 365

Asp Gly Leu His Ala Glu Val Thr Gly Val Gly Tyr Asn Gln Phe Gly  
370 375 380

Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn Pro Ala  
385 390 395 400

Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala Val Ile  
405 410 415

Arg Asn Asn Thr Leu Met Gly Lys Pro Thr Glu Gly Ala Leu Ile Ala  
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Leu Ala Met Lys Met Gly Leu Asp Gly Leu Gln Gln Asp Tyr Ile Arg  
435 440 445

Lys Ala Glu Tyr Pro Phe Ser Ser Glu Gln Lys Trp Met Ala Val Lys  
450 455 460

Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe Met Lys  
465 470 475 480

Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln Ser Lys  
485 490 495



645

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Ile Gly Val Ala Met Gly Gln Thr Gly Thr Asp Val Cys Lys Glu Ala

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665

670

Ala Asp Met Ile Leu Val Asp Asp Asp Phe Gln Thr Ile Met Ser Ala

675

680

685

Ile Glu Glu Gly Lys Gly Ile Tyr Asn Asn Ile Lys Asn Phe Val Arg

690

695

700

Phe Gln Leu Ser Thr Ser Ile Ala Ala Leu Thr Leu Ile Ser Leu Ala

705

710

715

720

Thr Leu Met Asn Phe Pro Asn Pro Leu Asn Ala Met Gln Ile Leu Trp

725

730

735

Ile Asn Ile Ile Met Asp Gly Pro Pro Ala Gln Ser Leu Gly Val Glu

740

745

750

Pro Val Asp Lys Asp Val Ile Arg Lys Pro Pro Arg Asn Trp Lys Asp

755

760

765

Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser Ser Ile

770

775

780

Ile Ile Val Cys Gly Thr Leu Phe Val Phe Trp Arg Glu Leu Arg Asp

785

790

795

800



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 Phe Asp Ile Ser Glu Asp Glu Pro Leu Trp Lys Lys Tyr Ile Ser Gln  
 65 70 75

ttt aaa aat ccc ctt att atg ctg ctt ctg gct tct gca gtc atc agt 708  
 Phe Lys Asn Pro Leu Ile Met Leu Leu Leu Ala Ser Ala Val Ile Ser  
 80 85 90

gtt tta atg cat cag ttt gat gat gcc gtc agt atc act gtg gca ata 756  
 Val Leu Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile  
 95 100 105 110

ctt atc gtt gtt aca gtt gcc ttt gtt cag gaa tat cgt tca gaa aaa 804  
 Leu Ile Val Val Thr Val Ala Phe Val Gln Glu Tyr Arg Ser Glu Lys  
 115 120 125

tct ctt gaa gaa ttg agt aaa ctt gtg cca cca gaa tgc cat tgt gtg 852  
 Ser Leu Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val  
 130 135 140

cgt gaa gga aaa ttg gag cat aca ctt gcc cga gac ttg gtt cca ggt 900  
 Arg Glu Gly Lys Leu Glu His Thr Leu Ala Arg Asp Leu Val Pro Gly  
 485/735



155

170

190

205

220

235

250

270

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Leu Gly Lys Asp Ile Leu Glu Met Phe Thr Ile Ser Val Ser Leu Ala  
290 295 300

gta gca gca att cct gaa ggt ctc ccc att gtg gtc aca gtg acg cta 1380  
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305 310 315

gct ctt ggt gtt atg aga atg gtg aag aaa agg gcc att gtg aaa aag 1428  
Ala Leu Gly Val Met Arg Met Val Lys Lys Arg Ala Ile Val Lys Lys  
320 325 330

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Leu Pro Ile Val Glu Thr Leu Gly Cys Cys Asn Val Ile Cys Ser Asp  
335 340 345 350

aaa act gga aca ctg acg aag aat gaa atg act gtt act cac ata ttt 1524  
Lys Thr Gly Thr Leu Thr Lys Asn Glu Met Thr Val Thr His Ile Phe  
355 360 365

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370 375 380

ttt ggg gaa gtg att gtt gat ggt gat gtt gtt cat gga ttc tat aac 1620  
Phe Gly Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn  
385 390 395

cca gct gtt agc aga att gtt gag gcg ggc tgt gtg tgc aat gat gct 1668  
Pro Ala Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala  
400 405 410

gta att aga aac aat act cta atg ggg aag cca aca gaa ggg gcc tta 1716  
Val Ile Arg Asn Asn Thr Leu Met Gly Lys Pro Thr Glu Gly Ala Leu  
415 420 425 430

att gct ctt gca atg aag atg ggt ctt gat gga ctt caa caa gac tac 1764  
Ile Ala Leu Ala Met Lys Met Gly Leu Asp Gly Leu Gln Gln Asp Tyr  
435 440 445

atc aga aaa gct gaa tac cct ttt agc tct gag caa aag tgg atg gct 1812  
Ile Arg Lys Ala Glu Tyr Pro Phe Ser Ser Glu Gln Lys Trp Met Ala  
450 455 460

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Val Lys Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe  
465 470 475

atg aaa ggt gct tac gaa caa gta att aag tac tgt act aca tac cag 1908  
Met Lys Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln  
480 485 490

agc aaa ggg cag acc ttg aca ctt act cag cag cag aga gat gtg tac 1956  
488/735

Ser Lys Gly Gln Thr Leu Thr Leu Thr Gln Gln Gln Arg Asp Val Tyr  
 495 500 505 510

caa caa gag aag gca cgc atg ggc tca gcg gga ctc aga gtt ctt gct 2004  
 Gln Gln Glu Lys Ala Arg Met Gly Ser Ala Gly Leu Arg Val Leu Ala  
 515 520 525

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 545 550 555

ctc att gcc tca gga gta tca ata aaa atg att act gga gat tca cag 2148  
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tcc cag tca gtc tca gga gaa gaa ata gat gca atg gat gtt cag cag 2244  
 Ser Gln Ser Val Ser Gly Glu Glu Ile Asp Ala Met Asp Val Gln Gln  
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 489/735

620

635

650

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gta gaa cca gtg gat aaa gat gtc att cgt aaa cct cct cgc aac tgg 2724  
 Val Glu Pro Val Asp Lys Asp Val Ile Arg Lys Pro Pro Arg Asn Trp  
 755 760 765

aaa gac agc att ttg act aaa aac ttg ata ctt aaa ata ctt gtt tca 2772  
 Lys Asp Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser  
 770 775 780

tca ata atc att gtt tgt ggg act ttg ttt gtc ttc tgg cgt gag cta 2820  
 Ser Ile Ile Ile Val Cys Gly Thr Leu Phe Val Phe Trp Arg Glu Leu  
 785 790 795

cga gac aat gtg att aca cct cga gac aca aca atg acc ttc aca tgc 2868  
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 Phe Val Phe Phe Asp Met Phe Asn Ala Leu Ser Ser Arg Ser Gln Thr  
 815 820 825 830

aag tct gtg ttt gag att gga ctc tgc agt aat aga atg ttt tgc tat 2964  
 Lys Ser Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr  
 835 840 845

gca gtt ctt gga tcc atc atg gga caa tta cta gtt att tac ttt cct 3012

Ala Val Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro

850

855

860

ccg ctt cag aag gtt ttt cag act gag agc cta agc ata ctg gat ctg 3060

Pro Leu Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu

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Leu Phe Leu Leu Gly Leu Thr Ser Ser Val Cys Ile Val Ala Glu Ile

880

885

890

ata aag aag gtt gaa agg agc agg gaa aag atc cag aag cat gtt agt 3156

Ile Lys Lys Val Glu Arg Ser Arg Glu Lys Ile Gln Lys His Val Ser

895

900

905

910

tcg aca tca tca tct ttt ctt gaa gta tgatgcatat tgcattatatt 3203

Ser Thr Ser Ser Ser Phe Leu Glu Val

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tgaagatttg agaacttttt aactattcat tgactaaaaa tgaacattaa tgttaaagac 3323

ttaagacttt aacctgctgg cagtcccaaa tgaaattatg caactttgat atcatattcc 3383

ttgatttaaa ttggcttttg tgattgagtg aaactttata aagcatatgg tcagttatatt 3443

aattaaaaag gcaaaacctg aaccaccttc tgcacttaaa gaagtctaac agtaciaaata 3503



Val Lys Asn Gly Ile Arg Thr Gly Phe Leu Glu Ile Asp Glu His Met  
 100 105 110

Arg Val Met Ser Glu Lys Lys His Gly Ala Asp Arg Ser Gly Ser Thr  
 115 120 125

Ala Val Gly Val Leu Ile Ser Pro Gln His Thr Tyr Phe Ile Asn Cys  
 130 135 140

Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn Arg Lys Val His Phe Phe  
 145 150 155 160

Thr Gln Asp His Lys Pro Ser Asn Pro Leu Glu Lys Glu Arg Ile Gln  
 165 170 175

Asn Ala Gly Gly Ser Val Met Ile Gln Arg Val Asn Gly Ser Leu Ala  
 180 185 190

Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr Lys Cys Val His Gly Lys  
 195 200 205

Gly Pro Thr Glu Gln Leu Val Ser Pro Glu Pro Glu Val His Asp Ile  
 210 215 220

Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile Ile Leu Ala Cys Asp Gly  
 225 230 235 240

Ile Trp Asp Val Met Gly Asn Glu Glu Leu Cys Asp Phe Val Arg Ser  
 494/735

245

250

255

Arg Leu Glu Val Thr Asp Asp Leu Glu Lys Val Cys Asn Glu Val Val

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Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp Asn Met Ser Val Ile Leu

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Ile Cys Phe Pro Asn Ala Pro Lys Val Ser Pro Glu Ala Val Lys Lys

290

295

300

Glu Ala Glu Leu Asp Lys Tyr Leu Glu Cys Arg Val Glu Glu Ile Ile

305

310

315

320

Lys Lys Gln Gly Glu Gly Val Pro Asp Leu Val His Val Met Arg Thr

325

330

335

Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro Pro Gly Gly Glu Leu Ala

340

345

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Ser Lys Arg Asn Val Ile Glu Ala Val Tyr Asn Arg Leu Asn Pro Tyr

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Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr Asp Asp Met Trp

370

375

380

<210> 136

<211> 2467

*(The following information was obtained from the records of the Federal Bureau of Investigation.)*



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agc agc atg caa ggc tgg cgt gtt gaa atg gag gat gca cat acg gct 569

Ser Ser Met Gln Gly Trp Arg Val Glu Met Glu Asp Ala His Thr Ala

30

35

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gtg atc ggt ttg cca agt gga ctt gaa tcg tgg tca ttc ttt gct gtg 617

Val Ile Gly Leu Pro Ser Gly Leu Glu Ser Trp Ser Phe Phe Ala Val

45

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tat gat ggg cat gct ggt tct cag gtt gcc aaa tac tgc tgt gag cat 665

Tyr Asp Gly His Ala Gly Ser Gln Val Ala Lys Tyr Cys Cys Glu His

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ttg tta gat cac atc acc aat aac cag gat ttt aaa ggg tct gca gga 713

Leu Leu Asp His Ile Thr Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly

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80

85

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gca cct tct gtg gaa aat gta aag aat gga atc aga aca ggt ttt ctg 761

Ala Pro Ser Val Glu Asn Val Lys Asn Gly Ile Arg Thr Gly Phe Leu

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gag att gat gaa cac atg aga gtt atg tca gag aag aaa cat ggt gca 809

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gat aga agt ggg tca aca gct gta ggt gtc tta att tct ccc caa cat 857

Asp Arg Ser Gly Ser Thr Ala Val Gly Val Leu Ile Ser Pro Gln His

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act tat ttc att aac tgt gga gac tca aga ggt tta ctt tgt agg aac 905

Thr Tyr Phe Ile Asn Cys Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn

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agg aaa gtt cat ttc ttc aca caa gat cac aaa cca agt aat ccg ctg 953

Arg Lys Val His Phe Phe Thr Gln Asp His Lys Pro Ser Asn Pro Leu

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gag aaa gaa cga att cag aat gca ggt ggc tct gta atg att cag cgt 1001

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175

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gtg aat ggc tct ctg gct gta tcg agg gcc ctt ggg gat ttt gat tac 1049

Val Asn Gly Ser Leu Ala Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr

190

195

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aaa tgt gtc cat gga aaa ggt cct act gag cag ctt gtc tca cca gag 1097

Lys Cys Val His Gly Lys Gly Pro Thr Glu Gln Leu Val Ser Pro Glu

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210

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cct gaa gtc cat gat att gaa aga tct gaa gaa gat gat cag ttc att 1145

Pro Glu Val His Asp Ile Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile

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Ile Leu Ala Cys Asp Gly Ile Trp Asp Val Met Gly Asn Glu Glu Leu

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tgt gat ttt gta aga tcc aga ctt gaa gtc act gat gac ctt gag aaa 1241



Cys Asp Phe Val Arg Ser Arg Leu Glu Val Thr Asp Asp Leu Glu Lys  
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gtt tgc aat gaa gta gtc gac acc tgt ttg tat aag gga agt cga gac 1289  
Val Cys Asn Glu Val Val Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp  
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Asn Met Ser Val Ile Leu Ile Cys Phe Pro Asn Ala Pro Lys Val Ser  
285 290 295

cca gaa gca gtg aag aag gag gca gag ttg gac aag tac ctg gaa tgc 1385  
Pro Glu Ala Val Lys Lys Glu Ala Glu Leu Asp Lys Tyr Leu Glu Cys  
300 305 310

aga gta gaa gaa atc ata aag aag cag ggg gaa ggc gtc ccc gac tta 1433  
Arg Val Glu Glu Ile Ile Lys Lys Gln Gly Glu Gly Val Pro Asp Leu  
315 320 325 330

gtc cat gtg atg cgc aca tta gcg agt gag aac atc ccc agc ctc cca 1481  
Val His Val Met Arg Thr Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro  
335 340 345

cca ggg ggt gaa ttg gca agc aag agg aat gtt att gaa gcc gtt tac 1529  
Pro Gly Gly Glu Leu Ala Ser Lys Arg Asn Val Ile Glu Ala Val Tyr  
350 355 360

aat aga ctg aat cct tac aaa aat gac gac act gac tct aca tca aca 1577  
Asn Arg Leu Asn Pro Tyr Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr

365

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gat gat atg tgg taaaactgct catctagcca tggagtttac cttcacctcc 1629  
Asp Asp Met Trp

380

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ggggatatga catgggtgag aatgattaca tcagagaact tcagcagtagc aacagctagc 1749

ccagaactga tttttttttt ttttttgtaa atttgagact tatgtaagcg tgatttcaaa 1809

ccataattcg tgttgtaaatt cagactccag caatttttgt tgtatgattt tgtttttttg 1869

taaagtgtaa ttgtccttgt acaaaatgct catatttaatt tatgaactgc tttaaatacac 1929

tatcaaagtt acaagaaatg tttggcttat tgtgtgatgc aacagatata tagccctttc 1989

aagtcattgtt gtgttttgac ttgggggttg aacagggaga gcagcagcca tgtcagctac 2049

acgctcaaatt gtgcagatga ttatggaaaa taacctcaaa atcttacaaa gctgaacatc 2109

caaggagtta ttgaaaacta tcttaaattgt tcttggtagg ggagttggca ttgttgataa 2169

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ttgcacctct tttcaagtcc ttacatttaa ttactaattg ataagcagca gcttcctaca 2349



Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser  
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Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser  
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Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met  
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Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala  
 145 150 155 160

Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser  
 165 170 175

Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr  
 180 185 190

Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln  
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Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln  
 210 215 220

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 502/735



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ctg aaa ctg aca tta ttt gtt aat ggc cag cca aga ccc ctt gaa tca 193

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agt cag gtg aaa tat ctc cgt cga gaa ctg ata gaa ctt cga aat aaa 241

Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys

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gtg aat cgt tta ttg gat agc ttg gaa cca cct gga gaa cca gga cct 289

Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro

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tcc acc aat att cct gaa aat gat act gtg gat ggt agg gaa gaa aag 337

Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys

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agt atg tct gct ttt gat cct tta aaa aac caa gat gaa atc aat aaa 433

Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys

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Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro

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cag caa cag gcc ggc tat ggt gca cag cag ccg cag gct cca cct cag 673

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Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln

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gcc tct caa cct gga atg gct cca agc caa cct ggg gcc tat caa cca 961

Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala Tyr Gln Pro

305

310

315

aga cca ggt ttt act tca ctt cct gga agt acc atg acc cct cct cca 1009

Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr Pro Pro Pro





330

345

355



Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val  
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Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu  
 165 170 175

Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val  
 180 185 190

Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp  
 195 200 205

Ser Ile Ala Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro  
 210 215 220

Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr  
 225 230 235 240

Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala  
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Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr  
 260 265 270

Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly  
 275 280 285

Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro  
 290 295 300

Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr

305 310 315 320

Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr

325 330 335

Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala

340 345 350

Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr

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<211> 1641

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (19).. (1206)

<400> 140

aacatcctgg agtccacc atg aac gga cag ttg gat cta agt ggg aag cta 51

Met Asn Gly Gln Leu Asp Leu Ser Gly Lys Leu

1 5 10

atc gtc aaa gct caa ctt ggg gag gat att cgg cga att cct att cat 99

Ile Val Lys Ala Gln Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His

15 20 25

aat gaa gat att act tat gat gaa tta gtg cta atg atg caa cga gtt 147

Asn Glu Asp Ile Thr Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val

30 35 40

ttc aga gga aaa ctt ctg agt aat gat gaa gta aca ata aag tat aaa 195

Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys

45 50 55

gat gaa gat gga gat ctt ata aca att ttt gat agt tct gac ctt tcc 243

Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser

60 65 70 75

ttt gca att cag tgc agt agg ata ctg aaa ctg aca tta ttt gtt aat 291

Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn

80 85 90

ggc cag cca aga ccc ctt gaa tca agt cag gtg aaa tat ctc cgt cga 339

Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg

95 100 105



Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln  
220 225 230 235

gca ggt cag atg tac caa cag tac cag caa cag gcc ggc tat ggt gca 771  
Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala  
240 245 250

cag cag ccg cag gct cca cct cag cag cct caa cag tat ggt att cag 819  
Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln  
255 260 265

tat tca gca agc tat agt cag cag act gga ccc caa caa cct cag cag 867  
Tyr Ser Ala Ser Tyr Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln  
270 275 280

ttc cag gga tat ggc cag caa cca act tcc cag gca cca gct cct gcc 915  
Phe Gln Gly Tyr Gly Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala  
285 290 295

ttt tct ggt cag cct caa caa ctg cct gct cag ccg cca cag cag tac 963  
Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr  
300 305 310 315

cag gcg agc aat tat cct gca caa act tac act gcc caa act tct cag 1011  
Gln Ala Ser Asn Tyr Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln  
320 325 330

cct act aat tat act gtg gct cct gcc tct caa cct gga atg gct cca 1059  
Pro Thr Asn Tyr Thr Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro  
513/735

335

340

345

agc caa cct ggg gcc tat caa cca aga cca ggt ttt act tca ctt cct 1107  
 Ser Gln Pro Gly Ala Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro  
 350 355 360

gga agt acc atg acc cct cct cca agt ggg cct aat cct tat gcg cgt 1155  
 Gly Ser Thr Met Thr Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg  
 365 370 375

aac cgt cct ccc ttt ggt cag gcc tat acc caa cct gga cct ggt tat 1203  
 Asn Arg Pro Pro Phe Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr  
 380 385 390 395

cga taaggaggct cctctacacc aattaatgta gctgctagct attggcctcc 1256  
 Arg

caaaagactc cagtactatt ttaatttgta ttgaagaagt tcagaaattt aaaagcagag 1316

cattttttat gatatacttg ttggtgttaa ttgaaagtat aatttgctgg aacacaaaga 1376

ccaaaatgaa agttttttcc tccctgctta aaaatgtagc agcttcttag ttactttgga 1436

acactactct tacatgtata aagtgattga cttgactttc tagcttcct tgtccgagg 1496

atattaaaat gctaggggtga ggtttagcca tcttacttgg ctttttacta ttaacatgat 1556

gtactaaagt agagcccttt gagaatacaa gatattatgt ataaaatgta acactgatga 1616



taggttaata aagatgattg aatcc

1641

<210> 141

<211> 323

<212> PRT

<213> Homo sapiens

<400> 141

Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro Ala Val Pro

1 5 10 15

Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu Gln Ile Thr

20 25 30

Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe Ala Val Asn

35 40 45

Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro

50 55 60

Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly

65 70 75 80

Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe Gln Lys Gly

85 90 95

Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp Phe Lys Val

100 105 110

515/735

Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg Val Pro Phe

115

120

125

His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln Leu Ser Tyr

130

135

140

Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro Ala Pro Ile

145

150

155

160

Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly Gln Met Phe

165

170

175

Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro Ala Tyr Pro

180

185

190

Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro Ser Lys Ser

195

200

205

Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg Phe His Ile

210

215

220

Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn Pro Arg Phe

225

230

235

240

Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn Ser Trp Gly

245

250

255

Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val Arg Gly Gln

260

265

270

Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu Lys Val Ala

275

280

285

Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu Arg Asn Leu

290

295

300

Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln Leu Thr His

305

310

315

320

Val Gln Thr

<210> 142

<211> 1616

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (72).. (1040)

<400> 142

aagtcgttcc ctctacaaag gacttcctag tgggtgtgaa aggcagcggg ggccacagag 60

gcggcggaga g atg gcc ttc agc ggt tcc cag gct ccc tac ctg agt cca 110

Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro



gtg ccc ttc cac cgt gtg gac acc atc tcc gtc aat ggc tct gtg cag 494

Val Pro Phe His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln

130

135

140

ctg tcc tac atc agc ttc cag cct ccc ggc gtg tgg cct gcc aac ccg 542

Leu Ser Tyr Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro

145

150

155

gct ccc att acc cag aca gtc atc cac aca gtg cag agc gcc cct gga 590

Ala Pro Ile Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly

160

165

170

cag atg ttc tct act ccc gcc atc cca cct atg atg tac ccc cac ccc 638

Gln Met Phe Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro

175

180

185

gcc tat ccg atg cct ttc atc acc acc att ctg gga ggg ctg tac cca 686

Ala Tyr Pro Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro

190

195

200

205

tcc aag tcc atc ctc ctg tca ggc act gtc ctg ccc agt gct cag agg 734

Ser Lys Ser Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg

210

215

220

ttc cac atc aac ctg tgc tct ggg aac cac atc gcc ttc cac ctg aac 782

Phe His Ile Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn

225

230

235



cagcacctgg ggctccagct gctggaatcc taccatccca ggaggcagge acagccaggg 1310

agaggggagg agtgggcagt gaagatgaag ccccatgctc agtccccctcc catccccccac 1370

gcagctccac cccagtcacca agccaccage tgtctgctcc tgggtgggagg tggcctcctc 1430

agccccctct ctctgacctt taacctcact ctcaccttgc accgtgcacc aacccttcac 1490

ccctcctgga aagcaggcct gatggcttcc cactggcctc caccacctga ccagagtgtt 1550

ctcttcagag gactggctcc tttcccagtg tccttaaaat aaagaaatga aaatgcttgt 1610

tggcac 1616

<210> 143

<211> 136

<212> PRT

<213> Homo sapiens

<400> 143

Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile

1

5

10

15

Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly

20

25

30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val





<400> 144

acaatcacag ctccgggcat tgggggaacc cgagccggct gcgccggggg aatccgtgcg 60

ggcgccttcc gtcccggtcc catcctcgcc gcgctccagc acctctgaag ttttgcagcg 120

cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180

aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236

Met Ala Gly Ala

1

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284

Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile

5 10 15 20

ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct 332

Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala

25 30 35

cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat 380

Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp

40 45 50

gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc 428

Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro

55 60 65

aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa 476

Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu  
70 75 80

att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac 524  
Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His  
85 90 95 100

atg gct ctt agc tgt ggt ttc ttg gac cag cgg cat gga cat ttg tca 572  
Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His Gly His Leu Ser  
105 110 115

gtt tgc ctt ctg acg gta gct ttt gga gga aga ttc ctg cag cca cta 620  
Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe Leu Gln Pro Leu  
120 125 130

atg cat tgt gta tgataacaaa aactctggta tgacacattt tctgtgatca 672  
Met His Cys Val  
135

ttgttaatta gtgacatagt aacatctgta gcagctgggt agtaaacctc atgtgggggt 732

ggggtggggg tgtattcctt gggggatggt ttgggccgaa tggggagtgg aatatttgac 792

atTTTTcctg ttttaaattc taggatagat tttaacatcc tttgcgggtcc cagtccaagg 852

taggctgggtg tcatagtctt ctcaactccta atccatgacc actgtttttt tcctatttat 912

atcaccagggt agcctactga gttaatatatt aagtgtgtcaa tagataagtg tccctgtttt 972

gtggcataat ataactgaat ttcatgagaa gatttattcc accaggggta tttcagcttt 1032

gaaaccaaat ctgtgtatct aatactaacc aatctgttgg atgtgggttt taaaaaatgt 1092

ttgctaaact acccaagtaa gatttactgt attaaatggc cttcgggtct gaaaagcttt 1152

tttaacctct tgcttaaaat gcgttttatt ttgataagat acttcaaata gcctccaaaa 1212

gtgtagatcc aatcacttaa ataaacctgt atgtatatgc 1252

- <210> 145
- <211> 468
- <212> PRT
- <213> Homo sapiens

<400> 145

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Cys Leu Gly Asp  
1 5 10 15

Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg Gln Phe Gln Phe  
20 25 30

Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln  
35 40 45

Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg  
50 55 60



Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile  
 225 230 235 240

Phe Cys Gly Glu His Met Met Asp Gln His Glu Arg Asn His Ile Ala  
 245 250 255

Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu  
 260 265 270

Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe  
 275 280 285

Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe  
 290 295 300

Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys  
 305 310 315 320

Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser  
 325 330 335

Leu Pro Ala Met Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile  
 340 345 350

Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met  
 355 360 365

Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys  
 527/735

370

375

380

Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile

385

390

395

400

Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala

405

410

415

Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu

420

425

430

Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr

435

440

445

Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala

450

455

460

Ala Ser Gly Ile

465

<210> 146

<211> 1943

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (379).. (1782)







atg gtg tgg tat tgg agg agg atc acc atg atg tcc cga ccc cca gtg 939  
Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val  
175 180 185

ctt ctg gaa aaa gtc atc ttt gcc ctt ggg att tcc atg acc ttt atc 987  
Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile  
190 195 200

aat atc cca gtg gaa tgg ttt tcc atc ggg ttt gac tgg acc tgg atg 1035  
Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met  
205 210 215

ctg ctg ttt ggt gac atc cga cag ggc atc ttc tat gcg atg ctt ctg 1083  
Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu  
220 225 230 235

tcc ttc tgg atc atc ttc tgt ggc gag cac atg atg gat cag cac gag 1131  
Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp Gln His Glu  
240 245 250

cgg aac cac atc gca ggg tat tgg aag caa gtc gga ccc att gcc gtt 1179  
Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val  
255 260 265

ggc tcc ttc tgc ctc ttc ata ttt gac atg tgt gag aga ggg gta caa 1227  
Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln  
270 275 280

ctc acg aat ccc ttc tac agt atc tgg act aca gac att gga aca gag 1275  
531/735

Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu  
 285 290 295

ctg gcc atg gcc ttc atc atc gtg gct gga atc tgc ctc tgc ctc tac 1323  
 Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr  
 300 305 310 315

ttc ctg ttt cta tgc ttc atg gta ttt cag gtg ttt cgg aac atc agt 1371  
 Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser  
 320 325 330

ggg aag cag tcc agc ctg cca gct atg agc aaa gtc cgg cgg cta cac 1419  
 Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg Arg Leu His  
 335 340 345

tat gag ggg cta att ttt agg ttc aag ttc ctc atg ctt atc acc ttg 1467  
 Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu  
 350 355 360

gcc tgc gct gcc atg act gtc atc ttc ttc atc gtt agt cag gta acg 1515  
 Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr  
 365 370 375

gaa ggc cat tgg aaa tgg ggc ggc gtc aca gtc caa gtg aac agt gcc 1563  
 Glu Gly His Trp Lys Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala  
 380 385 390 395

ttt ttc aca ggc atc tat ggg atg tgg aat ctg tat gtc ttt gct ctg 1611  
 Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu  
 532/735

atg ttc ttg tat gca cca tcc cat aaa aac tat gga gaa gac cag tcc

400

405

410

atg ttc ttg tat gca cca tcc cat aaa aac tat gga gaa gac cag tcc 1659  
Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser  
415 420 425

aat gga atg caa ctc cca tgt aaa tcg agg gaa gat tgt gct ttg ttt 1707  
Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe  
430 435 440

gtt tcg gaa ctt tat caa gaa ttg ttc agc gct tcg aaa tat tcc ttc 1755  
Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe  
445 450 455

atc aat gac aac gca gct tct ggt att tgagtcaaca aggcaacaca 1802  
Ile Asn Asp Asn Ala Ala Ser Gly Ile  
460 465

tgtttatcag ctttgcattt gcagttgtca cagtcacatt gattgtactt gtatacgcac 1862

acaaatacac tcatttagcc tttatctcaa aatgttaaataa ataaggaaaa aagcgtcaac 1922

aataaatatt ctttgagtat t 1943

- <210> 147
- <211> 460
- <212> PRT
- <213> Homo sapiens

<400> 147

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Cys Leu Gly Asp  
1 5 10 15

Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg Gln Phe Gln Gly  
20 25 30

Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr Phe Pro Ser Pro  
35 40 45

Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr  
50 55 60

Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr  
65 70 75 80

Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val  
85 90 95

Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu  
100 105 110

Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile  
115 120 125

Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly  
130 135 140

Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile  
145 150 155 160

Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg  
165 170 175

Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met  
180 185 190

Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp  
195 200 205

Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala  
210 215 220

Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp  
225 230 235 240

Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro  
245 250 255

Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg  
260 265 270

Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile  
275 280 285

Gly Thr Glu Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu  
290 295 300

Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg  
305 310 315 320

Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg  
325 330 335

Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu  
340 345 350

Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser  
355 360 365

Gln Val Thr Glu Gly His Trp Lys Trp Gly Gly Ile Thr Val Gln Val  
370 375 380

Asn Ser Ala Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val  
385 390 395 400

Phe Ala Leu Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu  
405 410 415

Asp Gln Ser Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys  
420 425 430

Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys  
435 440 445

Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile  
536/735

450

455

460

<210> 148

<211> 1919

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (376).. (1755)

<400> 148

atcacagctc cgggcattgg gggaaccga gccggctgcg ccgggggaat ccgtgcgggc 60

gccttcgctc ccggtcccat cctcgccgcg ctccagcacc tctgaagttt tgcagegccc 120

agaaaggagg cgaggaagga gggagtgtat gagaggagg agcaaaaagc tcaccctaaa 180

acatttatatt caaggagaaa agaaaaaggg ggggcgcaaa aatggctggg gcaattatag 240

aaaacatgag caccaagaag ctgtgcattg ttggtgggat tctgctcgtg ttccaaatca 300

tcgcctttct ggtgggaggc ttgattgctc cagggccac aacggcagtg tcctacatgt 360

cggtgaaatg tgtgg atg ccc gta aga acc atc aca aga caa aat ggt tcg 411

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser

1

5

10





Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His  
125 130 135 140

caa aat gga ggc ttc acc aag gtg tgg ttt gcc atg aag acc ttc ctt 843  
Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu  
145 150 155

acg ccc agc atc ttc atc att atg gtg tgg tat tgg agg agg atc acc 891  
Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr  
160 165 170

atg atg tcc cga ccc cca gtg ctt ctg gaa aaa gtc atc ttt gcc ctt 939  
Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu  
175 180 185

ggg att tcc atg acc ttt atc aat atc cca gtg gaa tgg ttt tcc atc 987  
Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile  
190 195 200

ggg ttt gac tgg acc tgg atg ctg ctg ttt ggt gac atc cga cag ggc 1035  
Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly  
205 210 215 220

atc ttc tat gcg atg ctt ctg tcc ttc tgg atc atc ttc tgt ggc gag 1083  
Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu  
225 230 235

cac atg atg gat cag cac gag cgg aac cac atc gca ggg tat tgg aag 1131  
His Met Met Asp Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys

240

245

250

caa gtc gga ccc att gcc gtt ggc tcc ttc tgc ctc ttc ata ttt gac 1179  
Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp

255

260

265

atg tgt gag aga ggg gta caa ctc acg aat ccc ttc tac agt atc tgg 1227  
Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp

270

275

280

act aca gac att gga aca gag ctg gcc atg gcc ttc atc atc gtg gct 1275  
Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe Ile Ile Val Ala  
285 290 295 300

gga atc tgc ctc tgc ctc tac ttc ctg ttt cta tgc ttc atg gta ttt 1323  
Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe  
305 310 315

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Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met  
320 325 330

agc aaa gtc cgg cgg cta cac tat gag ggg cta att ttt agg ttc aag 1419  
Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys  
335 340 345

ttc ctc atg ctt atc acc ttg gcc tgc gct gcc atg act gtc atc ttc 1467  
Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe  
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1919

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<211> 183

<212> PRT

<213> Homo sapiens

<400> 149

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro

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Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile

20

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30

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val

35

40

45

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val

50

55

60

Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr

65

70

75

80

Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu

85

90

95

Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val

100

105

110

542/735

Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn  
115 120 125

Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser  
130 135 140

Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala  
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Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe  
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Asp Arg His Lys Met Leu Ser  
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<211> 1562

<212> DNA

<213> Homo sapiens

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<400> 150

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gac cct ctg atc cga aag ccg gat gca tat act gag caa ctg cac aat 503

Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn

115

120

125

gag gag gag aat gag gat gct cgc tct atg gca gca gct gct gca tcc 551

Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser

130

135

140

ctc ggg gga ccc cga gca aac aca gtc ctg gag cgt gtg gaa ggt gcc 599

Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala

145

150

155

160

cag cag cgg tgg aag ctg cag gtg cag gag cag cgg aag aca gtc ttc 647

Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe

165

170

175

gat cgg cac aag atg ctc agc tagatgggct ggtgtggttg ggtcaaggcc 698

Asp Arg His Lys Met Leu Ser

180

ccaacacccat ggctgccagc ttccaggctg gacaaagcag ggggctactt ctcccttccc 758

tcggttccag tcttcccttt aaaagcctgt ggcatttttc ctcccttctcc ctaacttttag 818

aatgttgta cttggctatt ttgattaggg aagagggatg tggctctctga tctccgttgt 878

cttcttgggt ctttgggggt gaagggaggg ggaaggcagg ccagaaggga atggagacat 938

tcgaggcggc ctcaggagtg gatgcgatct gtctctcttg gctccactct tgccgccttc 998

cagctctgag tcttggaat gttgttacc ttggaagata aagctgggtc ttcaggaact 1058

cagtgtctgg gaggaagca tggcccagca ttcagcatgt gttcctttct gcagtgggtc 1118

tttatcacca cctccctccc agccccagcg cctcagcccc agccccagct ccagccctga 1178

ggacagctct gatgggagag ctgggcccc tgagccact gggctttcag ggtgcactgg 1238

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atctgaacac cacagccct gtacttgggt tgcctcttgt cctgaactt cgttgtacca 1478

gtgcatggag agaaaatttt gtctcttctg cttagagttg tgtgtaaatc aaggaagcca 1538

tcattaaatt gttttatttc tctc 1562

<210> 151

<211> 2815

<212> DNA

<213> Mus musculus

<220>



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DATE 08-09-2007 BY 60322 UCBAW



1. The first step in the process of identifying a problem is to recognize that a problem exists. This involves gathering information about the situation and identifying the specific issue that needs to be addressed.

aggctgtcgg ttcggaacat gtctccaccc accccaccct ctgtggctcc aggcttcatt 180

Met Asp Asn Pro Gly Pro Ser Leu Arg Gly Ala Phe Gly

att cta ggt gcc ttg gaa agg gac agg ctg acc cac ctg aaa cac aag 278

15                      20                      25

Leu Gly Ser Leu Cys Ser Gly Ser Gln Glu Ser Lys Leu Leu His Ala

atg gta ctc ctg gct ctg ggc cag gac acg gag gcc agg gtc tct ctg 374

50                      55                      60

Glu Ser Leu Lys Met Asn Thr Val Ala Gln Leu Val Ala His Gln Trp

547/735

gca gac atg gag acc aca gag ggc cct gag gag cct cca gac ttg tcc 470

Ala Asp Met Glu Thr Thr Glu Gly Pro Glu Glu Pro Pro Asp Leu Ser

80

85

90

tgg acg gtg gct cgc ctg tac cac ctg ctg gct gag gag aac ctg tgt 518

Trp Thr Val Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Asn Leu Cys

95

100

105

ccg gcc tct aca agg gac atg gct tac cag gtg gcc ctt cgt gac ttt 566

Pro Ala Ser Thr Arg Asp Met Ala Tyr Gln Val Ala Leu Arg Asp Phe

110

115

120

125

gcc tcc cag ggt gac cac cag ctg ggc caa ctc cag aat gag gcc tgg 614

Ala Ser Gln Gly Asp His Gln Leu Gly Gln Leu Gln Asn Glu Ala Trp

130

135

140

gat cgg tgc agt tca gat atc aag ggg gac ccc agt ggt ttc cag cca 662

Asp Arg Cys Ser Ser Asp Ile Lys Gly Asp Pro Ser Gly Phe Gln Pro

145

150

155

ctc cat tct cat cag ggt tcc ctg cag cca cct tca gca tcc cct gca 710

Leu His Ser His Gln Gly Ser Leu Gln Pro Pro Ser Ala Ser Pro Ala

160

165

170

gtg acc aga agc cag cct cgt ccc att gac aca cca gac tgg agt tgg 758

Val Thr Arg Ser Gln Pro Arg Pro Ile Asp Thr Pro Asp Trp Ser Trp

175

180

185

gga cat acg tta cac tcc acc aac agc act gcc tca ctg gcc agc cac 806  
 Gly His Thr Leu His Ser Thr Asn Ser Thr Ala Ser Leu Ala Ser His  
 190 195 200 205

cta gag atc agc cag tca ccc act ctt gcc ttt ctc tct tca cac cat 854  
 Leu Glu Ile Ser Gln Ser Pro Thr Leu Ala Phe Leu Ser Ser His His  
 210 215 220

gga acc cat ggg ccc agc aag cta tgt aac aca ccg ctg gac act cag 902  
 Gly Thr His Gly Pro Ser Lys Leu Cys Asn Thr Pro Leu Asp Thr Gln  
 225 230 235

gag cct cag ctt gtc cct gaa ggc tgc caa gaa cct gag gag ata agc 950  
 Glu Pro Gln Leu Val Pro Glu Gly Cys Gln Glu Pro Glu Glu Ile Ser  
 240 245 250

tgg cct cca tca gtg gag acc agt gtc tcc tta ggg tta cca cac gaa 998  
 Trp Pro Pro Ser Val Glu Thr Ser Val Ser Leu Gly Leu Pro His Glu  
 255 260 265

att agc gtt cca gag gtg tct cca gag gag gct tcg ccc atc ctc cct 1046  
 Ile Ser Val Pro Glu Val Ser Pro Glu Glu Ala Ser Pro Ile Leu Pro  
 270 275 280 285

gac gcc ctg gct gct cca gac aca agt gtc cac tgt ccc att gaa tgc 1094  
 Asp Ala Leu Ala Ala Pro Asp Thr Ser Val His Cys Pro Ile Glu Cys  
 290 295 300

aca gag ttg tct aca aac tcc agg tct ccc ctg acg tcc acc aca gaa 1142  
 549/735

Thr Glu Leu Ser Thr Asn Ser Arg Ser Pro Leu Thr Ser Thr Thr Glu  
305 310 315

agt gtt gga aag cag tgg cct att aca agt cag agg tca cct cag gtt 1190  
Ser Val Gly Lys Gln Trp Pro Ile Thr Ser Gln Arg Ser Pro Gln Val  
320 325 330

cct gta gga gat gat tct ctg cag aac acc acg tca tcc agc cct cct 1238  
Pro Val Gly Asp Asp Ser Leu Gln Asn Thr Thr Ser Ser Ser Pro Pro  
335 340 345

gcc cag cca cca tcc ctc caa gcc tcc cct aag ctg cct cct tcc cct 1286  
Ala Gln Pro Pro Ser Leu Gln Ala Ser Pro Lys Leu Pro Pro Ser Pro  
350 355 360 365

ctg tcc tct gct tcc tcc ccg agc agc tac cct gct cct cca<sup>y</sup> acc tcc 1334  
Leu Ser Ser Ala Ser Ser Pro Ser Ser Tyr Pro Ala Pro Pro Thr Ser  
370 375 380

aca tcc cct gtt ttg gac cac tca gaa aca tct gat cag aaa ttc tat 1382  
Thr Ser Pro Val Leu Asp His Ser Glu Thr Ser Asp Gln Lys Phe Tyr  
385 390 395

aac ttt gtg gtt atc cat gcc agg gct gat gaa cag gtg gcc cta cgt 1430  
Asn Phe Val Val Ile His Ala Arg Ala Asp Glu Gln Val Ala Leu Arg  
400 405 410

att cgg gag aag ctg gag acc ctc ggg gta cct gac ggg gcc acc ttc 1478  
Ile Arg Glu Lys Leu Glu Thr Leu Gly Val Pro Asp Gly Ala Thr Phe  
550/735

|  |     |     |     |
|--|-----|-----|-----|
| 415  | 420 | 425 |     |
| tgt gag gaa ttt cag gtg ccc ggg cgt ggt gag ctg cac tgt ctc caa 1526 |     |     |     |
| Cys Glu Glu Phe Gln Val Pro Gly Arg Gly Glu Leu His Cys Leu Gln      |     |     |     |
| 430  | 435 | 440 | 445 |
| gat gcc atc gat cac tcg ggg ttc acg atc ctg ctc ctg act gct agc 1574 |     |     |     |
| Asp Ala Ile Asp His Ser Gly Phe Thr Ile Leu Leu Leu Thr Ala Ser      |     |     |     |
|  | 450 | 455 | 460 |
| ttt gat tgc agc ctg agc ctg cat caa atc aac cat gct ctc atg aac 1622 |     |     |     |
| Phe Asp Cys Ser Leu Ser Leu His Gln Ile Asn His Ala Leu Met Asn      |     |     |     |
|  | 465 | 470 | 475 |
| agc ctt aca cag tct ggg agg cag gac tgt gtg atc ccc ctc ctc cca 1670 |     |     |     |
| Ser Leu Thr Gln Ser Gly Arg Gln Asp Cys Val Ile Pro Leu Leu Pro      |     |     |     |
|  | 480 | 485 | 490 |
| ctt gag tgt tcc cag gcc cag ctc agc cca gat aca acc aga ctg ctc 1718 |     |     |     |
| Leu Glu Cys Ser Gln Ala Gln Leu Ser Pro Asp Thr Thr Arg Leu Leu      |     |     |     |
|  | 495 | 500 | 505 |
| cac agc att gtg tgg ctg gat gaa cac tcc cca atc ttc gcc aga aag 1766 |     |     |     |
| His Ser Ile Val Trp Leu Asp Glu His Ser Pro Ile Phe Ala Arg Lys      |     |     |     |
| 510  | 515 | 520 | 525 |
| gtg gca aac acc ttc aag aca cag aag ctc cag gca cag cgg gta cgc 1814 |     |     |     |
| Val Ala Asn Thr Phe Lys Thr Gln Lys Leu Gln Ala Gln Arg Val Arg      |     |     |     |
|  | 530 | 535 | 540 |

tgg aag aaa gcg cag gag gcc aga acc ctc aag gag cag agc ata cag 1862

Trp Lys Lys Ala Gln Glu Ala Arg Thr Leu Lys Glu Gln Ser Ile Gln

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550

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ctg gag gca gag cgg caa aac gtg gca gcc ata tct gct gcc tac aca 1910

Leu Glu Ala Glu Arg Gln Asn Val Ala Ala Ile Ser Ala Ala Tyr Thr

560

565

570

gcc tat gtc cat agc tat agg gcc tgg caa gca gag atg aac aaa ctt 1958

Ala Tyr Val His Ser Tyr Arg Ala Trp Gln Ala Glu Met Asn Lys Leu

575

580

585

ggg gtg gct ttt ggg aag aac ttg tca ctg ggg act cca aca ccc agc 2006

Gly Val Ala Phe Gly Lys Asn Leu Ser Leu Gly Thr Pro Thr Pro Ser

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600

605

tgg ccc gga tgt cca cag cca ata cct tct cat cct cag ggt ggt act 2054

Trp Pro Gly Cys Pro Gln Pro Ile Pro Ser His Pro Gln Gly Gly Thr

610

615

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cca gtt ttc ccc tat tcc cca cag cct cca tcc ttc cct cag cct cca 2102

Pro Val Phe Pro Tyr Ser Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro

625

630

635

tgc ttc cct cag cct cca tcc ttc cct cag cct cca tcc ttc cca ctg 2150

Cys Phe Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro Ser Phe Pro Leu

640

645

650

cct cca gtc tct tcc cca cag tcc caa tcc ttt cca tca gcc tcc tcc 2198

Pro Pro Val Ser Ser Pro Gln Ser Gln Ser Phe Pro Ser Ala Ser Ser

655

660

665

cca gcc cca cag act cca gga cct cag cct ctc att att cac cat gcc 2246

Pro Ala Pro Gln Thr Pro Gly Pro Gln Pro Leu Ile Ile His His Ala

670

675

680

685

cag atg gtt cag ctg ggt gtc aac aat cac atg tgg ggc cac aca ggg 2294

Gln Met Val Gln Leu Gly Val Asn Asn His Met Trp Gly His Thr Gly

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695

700

gcc cag tca tct gat gac aag act gag tgt tcg gag aac ccc tgt atg 2342

Ala Gln Ser Ser Asp Asp Lys Thr Glu Cys Ser Glu Asn Pro Cys Met

705

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ggc cct ctg act gat cag ggc gaa ccc ctt ctt gag act cca gag 2387

Gly Pro Leu Thr Asp Gln Gly Glu Pro Leu Leu Glu Thr Pro Glu

720

725

730

tgaccaggtt ggaccccacc tagatggcta gagtgacaag attggacttc acctgggtcc 2447

ttaaaatgat agtggaggaa gggaacctcg cctgggtccc cagagtagcc agaggactta 2507

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<212> PRT

<213> Mus musculus

<400> 152

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Leu Cys Ser Gly Ser Gln Glu Ser Lys Leu Leu His Ala Met Val Leu  
35 40 45

Leu Ala Leu Gly Gln Asp Thr Glu Ala Arg Val Ser Leu Glu Ser Leu  
50 55 60

Lys Met Asn Thr Val Ala Gln Leu Val Ala His Gln Trp Ala Asp Met  
65 70 75 80







385 390 395 400

Val Ile His Ala Arg Ala Asp Glu Gln Val Ala Leu Arg Ile Arg Glu  
405 410 415

Lys Leu Glu Thr Leu Gly Val Pro Asp Gly Ala Thr Phe Cys Glu Glu  
420 425 430

Phe Gln Val Pro Gly Arg Gly Glu Leu His Cys Leu Gln Asp Ala Ile  
435 440 445

Asp His Ser Gly Phe Thr Ile Leu Leu Leu Thr Ala Ser Phe Asp Cys  
450 455 460

Ser Leu Ser Leu His Gln Ile Asn His Ala Leu Met Asn Ser Leu Thr  
465 470 475 480

Gln Ser Gly Arg Gln Asp Cys Val Ile Pro Leu Leu Pro Leu Glu Cys  
485 490 495

Ser Gln Ala Gln Leu Ser Pro Asp Thr Thr Arg Leu Leu His Ser Ile  
500 505 510

Val Trp Leu Asp Glu His Ser Pro Ile Phe Ala Arg Lys Val Ala Asn  
515 520 525

Thr Phe Lys Thr Gln Lys Leu Gln Ala Gln Arg Val Arg Trp Lys Lys  
530 535 540

Ala Gln Glu Ala Arg Thr Leu Lys Glu Gln Ser Ile Gln Leu Glu Ala  
545 550 555 560

Glu Arg Gln Asn Val Ala Ala Ile Ser Ala Ala Tyr Thr Ala Tyr Val  
565 570 575

His Ser Tyr Arg Ala Trp Gln Ala Glu Met Asn Lys Leu Gly Val Ala  
580 585 590

Phe Gly Lys Asn Leu Ser Leu Gly Thr Pro Thr Pro Ser Trp Pro Gly  
595 600 605

Cys Pro Gln Pro Ile Pro Ser His Pro Gln Gly Gly Thr Pro Val Phe  
610 615 620

Pro Tyr Ser Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro Cys Phe Pro  
625 630 635 640

Gln Pro Pro Ser Phe Pro Gln Pro Pro Ser Phe Pro Leu Pro Pro Val  
645 650 655

Ser Ser Pro Gln Ser Gln Ser Phe Pro Ser Ala Ser Ser Pro Ala Pro  
660 665 670

Gln Thr Pro Gly Pro Gln Pro Leu Ile Ile His His Ala Gln Met Val  
675 680 685

Gln Leu Gly Val Asn Asn His Met Trp Gly His Thr Gly Ala Gln Ser  
690 695 700



ctc ttg tat ctg aag cac aaa ctg aag acc cca cgc cca ggc tgc cag 210

Leu Leu Tyr Leu Lys His Lys Leu Lys Thr Pro Arg Pro Gly Cys Gln

25

30

35

ggg cag gac ctc ctg cat gcc atg gtt ctc ctg aag ctg ggc cag gaa 258

Gly Gln Asp Leu Leu His Ala Met Val Leu Leu Lys Leu Gly Gln Glu

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45

50

act gag gcc agg atc tct cta gag gca ttg aag gcc gat gcg gtg gcc 306

Thr Glu Ala Arg Ile Ser Leu Glu Ala Leu Lys Ala Asp Ala Val Ala

55

60

65

70

cgg ctg gtg gcc cgc cag tgg gct ggc gtg gac agc acc gag gac cca 354

Arg Leu Val Ala Arg Gln Trp Ala Gly Val Asp Ser Thr Glu Asp Pro

75

80

85

gag gag ccc cca gat gtg tcc tgg gct gtg gcc cgc ttg tac cac ctg 402

Glu Glu Pro Pro Asp Val Ser Trp Ala Val Ala Arg Leu Tyr His Leu

90

95

100

ctg gct gag gag aag ctg tgc ccc gcc tcg ctg cgg gac gtg gcc tac 450

Leu Ala Glu Glu Lys Leu Cys Pro Ala Ser Leu Arg Asp Val Ala Tyr

105

110

115

cag gaa gcc gtc cgc acc ctc agc tcc agg gac gac cac cgg ctg ggg 498

Gln Glu Ala Val Arg Thr Leu Ser Ser Arg Asp Asp His Arg Leu Gly

120

125

130

gaa ctt cag gat gag gcc cga aac cgg tgt ggg tgg gac att gct ggg 546







cac ctg acc ccc tcc tcc ctg ttc cct tcc tcc ctg gaa tca tca tcg 1266  
 His Leu Thr Pro Ser Ser Leu Phe Pro Ser Ser Leu Glu Ser Ser Ser  
 375 380 385 390

gaa cag aaa ttc tat aac ttt gtg atc ctc cac gcc agg gca gac gaa 1314  
 Glu Gln Lys Phe Tyr Asn Phe Val Ile Leu His Ala Arg Ala Asp Glu  
 395 400 405

cac atc gcc ctg cgg gtt cgg gag aag ctg gag gcc ctt ggc gtg ccc 1362  
 His Ile Ala Leu Arg Val Arg Glu Lys Leu Glu Ala Leu Gly Val Pro  
 410 415 420

gac ggg gcc acc ttc tgc gag gat ttc cag gtg ccg ggg cgc ggg gag 1410  
 Asp Gly Ala Thr Phe Cys Glu Asp Phe Gln Val Pro Gly Arg Gly Glu  
 425 430 435

ctg agc tgc ctg cag gac gcc ata gac cac tca gct ttc atc atc cta 1458  
 Leu Ser Cys Leu Gln Asp Ala Ile Asp His Ser Ala Phe Ile Ile Leu  
 440 445 450

ctt ctc acc tcc aac ttc gac tgt cgc ctg agc ctg cac cag gtg aac 1506  
 Leu Leu Thr Ser Asn Phe Asp Cys Arg Leu Ser Leu His Gln Val Asn  
 455 460 465 470

caa gcc atg atg agc aac ctc acg cga cag ggg tcg cca gac tgt gtc 1554  
 Gln Ala Met Met Ser Asn Leu Thr Arg Gln Gly Ser Pro Asp Cys Val  
 475 480 485

Ile Pro Phe Leu Pro Leu Glu Ser Ser Pro Ala Gln Leu Ser Ser Asp  
490 495 500

acg gcc agc ctg ctc tcc ggg ctg gtg cgg ctg gac gaa cac tcc cag 1650  
Thr Ala Ser Leu Leu Ser Gly Leu Val Arg Leu Asp Glu His Ser Gln  
505 510 515

atc ttc gcc agg aag gtg gcc aac acc ttc aag ccc cac agg ctt cag 1698  
Ile Phe Ala Arg Lys Val Ala Asn Thr Phe Lys Pro His Arg Leu Gln  
520 525 530

gcc cga aag gcc atg tgg agg aag gaa cag gac acc cga gcc ctg cgg 1746  
Ala Arg Lys Ala Met Trp Arg Lys Glu Gln Asp Thr Arg Ala Leu Arg  
535 540 545 550

gaa cag agc caa cac ctg gac ggt gag cgg atg cag gcg gcg gca ctg 1794  
Glu Gln Ser Gln His Leu Asp Gly Glu Arg Met Gln Ala Ala Ala Leu  
555 560 565

aac gca gcc tac tca gcc tac ctc cag agc tac ttg tcc tac cag gca 1842  
Asn Ala Ala Tyr Ser Ala Tyr Leu Gln Ser Tyr Leu Ser Tyr Gln Ala  
570 575 580

cag atg gag cag ctc cag gtg gct ttt ggg agc cac atg tca ttt ggg 1890  
Gln Met Glu Gln Leu Gln Val Ala Phe Gly Ser His Met Ser Phe Gly  
585 590 595

act ggg gcg ccc tat ggg gct cga atg ccc ttt ggg ggc cag gtg ccc 1938  
564/735

Thr Gly Ala Pro Tyr Gly Ala Arg Met Pro Phe Gly Gly Gln Val Pro  
600 605 610

ctg gga gcc ccg cca ccc ttt ccc act tgg ccg ggg tgc ccg cag ccg 1986  
Leu Gly Ala Pro Pro Pro Phe Pro Thr Trp Pro Gly Cys Pro Gln Pro  
615 620 625 630

cca ccc ctg cac gca tgg cag gct ggc acc ccc cca ccg ccc tcc cca 2034  
Pro Pro Leu His Ala Trp Gln Ala Gly Thr Pro Pro Pro Pro Ser Pro  
635 640 645

cag cca gca gcc ttt cca cag tca ctg ccc ttc ccg cag tcc cca gcc 2082  
Gln Pro Ala Ala Phe Pro Gln Ser Leu Pro Phe Pro Gln Ser Pro Ala  
650 655 660

ttc cct acg gcc tca ccc gca ccc cct cag agc cca ggg ctg caa ccc 2130  
Phe Pro Thr Ala Ser Pro Ala Pro Pro Gln Ser Pro Gly Leu Gln Pro  
665 670 675

ctc att atc cac cac gca cag atg gta cag ctg ggg ctg aac aac cac 2178  
Leu Ile Ile His His Ala Gln Met Val Gln Leu Gly Leu Asn Asn His  
680 685 690

atg tgg aac cag aga ggg tcc cag gcg ccc gag gac aag acg cag gag 2226  
Met Trp Asn Gln Arg Gly Ser Gln Ala Pro Glu Asp Lys Thr Gln Glu  
695 700 705 710

gca gaa tgaccgcgtg tccttgccctg accacctggg gaacacccct ggaccaggc 2282  
Ala Glu



Lys Ala Asp Ala Val Ala Arg Leu Val Ala Arg Gln Trp Ala Gly Val  
65 70 75 80

Asp Ser Thr Glu Asp Pro Glu Glu Pro Pro Asp Val Ser Trp Ala Val  
85 90 95

Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Lys Leu Cys Pro Ala Ser  
100 105 110

Leu Arg Asp Val Ala Tyr Gln Glu Ala Val Arg Thr Leu Ser Ser Arg  
115 120 125

Asp Asp His Arg Leu Gly Glu Leu Gln Asp Glu Ala Arg Asn Arg Cys  
130 135 140

Gly Trp Asp Ile Ala Gly Asp Pro Gly Ser Ile Arg Thr Leu Gln Ser  
145 150 155 160

Asn Leu Gly Cys Leu Pro Pro Ser Ser Ala Leu Pro Ser Gly Thr Arg  
165 170 175

Ser Leu Pro Arg Pro Ile Asp Gly Val Ser Asp Trp Ser Gln Gly Cys  
180 185 190

Ser Leu Arg Ser Thr Gly Ser Pro Ala Ser Leu Ala Ser Asn Leu Glu  
195 200 205

Ile Ser Gln Ser Pro Thr Met Pro Phe Leu Ser Leu His Arg Ser Pro  
567/735

210 215 220

His Gly Pro Ser Lys Leu Cys Asp Asp Pro Gln Ala Ser Leu Val Pro  
 225 230 235 240

Glu Pro Val Pro Gly Gly Cys Gln Glu Pro Glu Glu Met Ser Trp Pro  
 245 250 255

Pro Ser Gly Glu Ile Ala Ser Pro Pro Glu Leu Pro Ser Ser Pro Pro  
 260 265 270

Pro Gly Leu Pro Glu Val Ala Pro Asp Ala Thr Ser Thr Gly Leu Pro  
 275 280 285

Asp Thr Pro Ala Ala Pro Glu Thr Ser Thr Asn Tyr Pro Val Glu Cys  
 290 295 300

Thr Glu Gly Ser Ala Gly Pro Gln Ser Leu Pro Leu Pro Ile Leu Glu  
 305 310 315 320

Pro Val Lys Asn Pro Cys Ser Val Lys Asp Gln Thr Pro Leu Gln Leu  
 325 330 335

Ser Val Glu Asp Thr Thr Ser Pro Asn Thr Lys Pro Cys Pro Pro Thr  
 340 345 350

Pro Thr Thr Pro Glu Thr Ser Pro Pro Pro Pro Pro Pro Pro Ser  
 355 360 365

Ser Thr Pro Cys Ser Ala His Leu Thr Pro Ser Ser Leu Phe Pro Ser  
370 375 380

Ser Leu Glu Ser Ser Ser Glu Gln Lys Phe Tyr Asn Phe Val Ile Leu  
385 390 395 400

His Ala Arg Ala Asp Glu His Ile Ala Leu Arg Val Arg Glu Lys Leu  
405 410 415

Glu Ala Leu Gly Val Pro Asp Gly Ala Thr Phe Cys Glu Asp Phe Gln  
420 425 430

Val Pro Gly Arg Gly Glu Leu Ser Cys Leu Gln Asp Ala Ile Asp His  
435 440 445

Ser Ala Phe Ile Ile Leu Leu Leu Thr Ser Asn Phe Asp Cys Arg Leu  
450 455 460

Ser Leu His Gln Val Asn Gln Ala Met Met Ser Asn Leu Thr Arg Gln  
465 470 475 480

Gly Ser Pro Asp Cys Val Ile Pro Phe Leu Pro Leu Glu Ser Ser Pro  
485 490 495

Ala Gln Leu Ser Ser Asp Thr Ala Ser Leu Leu Ser Gly Leu Val Arg  
500 505 510

Leu Asp Glu His Ser Gln Ile Phe Ala Arg Lys Val Ala Asn Thr Phe  
515 520 525

Lys Pro His Arg Leu Gln Ala Arg Lys Ala Met Trp Arg Lys Glu Gln  
530 535 540

Asp Thr Arg Ala Leu Arg Glu Gln Ser Gln His Leu Asp Gly Glu Arg  
545 550 555 560

Met Gln Ala Ala Ala Leu Asn Ala Ala Tyr Ser Ala Tyr Leu Gln Ser  
565 570 575

Tyr Leu Ser Tyr Gln Ala Gln Met Glu Gln Leu Gln Val Ala Phe Gly  
580 585 590

Ser His Met Ser Phe Gly Thr Gly Ala Pro Tyr Gly Ala Arg Met Pro  
595 600 605

Phe Gly Gly Gln Val Pro Leu Gly Ala Pro Pro Pro Phe Pro Thr Trp  
610 615 620

Pro Gly Cys Pro Gln Pro Pro Pro Leu His Ala Trp Gln Ala Gly Thr  
625 630 635 640

Pro Pro Pro Pro Ser Pro Gln Pro Ala Ala Phe Pro Gln Ser Leu Pro  
645 650 655

Phe Pro Gln Ser Pro Ala Phe Pro Thr Ala Ser Pro Ala Pro Pro Gln  
660 665 670

Ser Pro Gly Leu Gln Pro Leu Ile Ile His His Ala Gln Met Val Gln  
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Met Lys Lys Lys Ser

1 5

ctg ggg gag gtg ctg ctg cct gta ttt gaa agg aag ggc att gcg ctg 343  
Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg Lys Gly Ile Ala Leu  
10 15 20

ggc aaa gtg gac atc tac ctg gac cag tcc aac aca ccc ctg tcc etc 391  
Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn Thr Pro Leu Ser Leu  
25 30 35

acc ttc gag gcc tac agg ttc ggg gga cac tac ctt cgt gtc aaa gcc 439  
Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr Leu Arg Val Lys Ala  
40 45 50

cca gcc aag cct gga gat gag ggc aag gtg gag cag ggc atg aag gac 487  
Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu Gln Gly Met Lys Asp  
55 60 65

tcc aag tcc ctg agt ttg ccg att ctg cgg cca gct ggg acc ggg ccc 535  
Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro Ala Gly Thr Gly Pro  
70 75 80 85

ccc gcc ctg gag cgt gtg gac gcc cag agc cgc cgg gag agc ctg gac 583  
Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg Arg Glu Ser Leu Asp  
90 95 100

atc ttg gcc cct ggc cgc cgc cgc aag aac atg tcg gag ttc ctg ggg 631  
Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met Ser Glu Phe Leu Gly

105

110

115

gag gcg agc atc ccc ggg cag gag ccc ccc acg ccc tcc agc tgc tct 679  
 Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr Pro Ser Ser Cys Ser  
 120 125 130

ctg ccc agc ggc agc agt ggc agc acc aac act ggc gac agc tgg aag 727  
 Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr Gly Asp Ser Trp Lys  
 135 140 145

aac cgg gcg gcc agt cgc ttc agc ggc ttt ttc agc tcc ggc ccc agc 775  
 Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe Ser Ser Gly Pro Ser  
 150 155 160 165

acc agc gcc ttt ggc cgg gag gta gac aag atg gag cag ctg gag ggc 823  
 Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met Glu Gln Leu Glu Gly  
 170 175 180

aag ctg cac acc tac agc ctc ttc ggg ctg ccc agg ctg ccc cgg ggc 871  
 Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro Arg Leu Pro Arg Gly  
 185 190 195

ctg cgc ttc gac cat gac tcc tgg gag gag gag tac gat gaa gac gag 919  
 Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu Tyr Asp Glu Asp Glu  
 200 205 210

gat gag gac aat gcc tgc ctg agg ctg gag gac agc tgg cgg gag ctc 967  
 Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp Ser Trp Arg Glu Leu  
 215 220 225



atc cgc tac tgc atg gag gag gag ggc tgc atg gag tac atg cgc ggc 1351

Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met Glu Tyr Met Arg Gly

345

350

355

ctg ctg cgc gac aac gac ctc ttc cgg gcc tac atc acg tgg gcg gag 1399

Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr Ile Thr Trp Ala Glu

360

365

370

aag cac cca cag tgc cag agg ctg aag ctg agc gac atg ctg gcc aaa 1447

Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser Asp Met Leu Ala Lys

375

380

385

ccc cac cag cgg ctc acc aag tac ccg ctg ctg ctc aag tcg gtg ctg 1495

Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu Leu Lys Ser Val Leu

390

395

400

405

agg aag acc gag gag ccg cgc gcc aag gag gcc gtc gtc gcc atg atc 1543

Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala Val Val Ala Met Ile

410

415

420

ggc tcc gtg gag cgc ttc atc cac cac gtg aac gcg tgc atg cgg cag 1591

Gly Ser Val Glu Arg Phe Ile His His Val Asn Ala Cys Met Arg Gln

425

430

435

cgg cag gag cgg cag cgg ctg gcg gcc gtg gtg agc cgc atc gac gcc 1639

Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val Ser Arg Ile Asp Ala

440

445

450

tac gag gtg gtg gaa agc agc agc gac gaa gtg gac aag ctc ctg aag 1687



570

575

580

gtg gac acc att tac aat gcc cag aac cag ctg caa cag ctg cgt gca 2071  
Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu Gln Gln Leu Arg Ala

585

590

595

cag gag ccc cca ggc agt cag cag ccc ctg cag agc ctg gaa gag gag 2119  
Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln Ser Leu Glu Glu Glu

600

605

610

gag gat gag cag gag gag gaa gag gag gag gag gag gag gag gag gaa 2167  
Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu

615

620

625

ggc gag gac agt ggc act tca gct gcc agc tcc cct acc atc atg cgg 2215  
Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser Pro Thr Ile Met Arg

630

635

640

645

aaa agc agc ggc agc ccc gac tct cag cac tgt gcc tca gat ggc tcc 2263  
Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys Ala Ser Asp Gly Ser

650

655

660

acg gag acc ctg gcc atg gtt gtg gta gag cct ggg gac acg ctg tcc 2311  
Thr Glu Thr Leu Ala Met Val Val Val Glu Pro Gly Asp Thr Leu Ser

665

670

675

tcc ccc gag ttc gac agc ggt cct ttc agc tcc cag tct gat gag acc 2359  
Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser Gln Ser Asp Glu Thr

680

685

690









Leu Arg Val Lys Ala Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu

50

55

60

Gln Gly Met Lys Asp Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro

65

70

75

80

Ala Gly Thr Gly Pro Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg

85

90

95

Arg Glu Ser Leu Asp Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met

100

105

110

Ser Glu Phe Leu Gly Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr

115

120

125

Pro Ser Ser Cys Ser Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr

130

135

140

Gly Asp Ser Trp Lys Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe

145

150

155

160

Ser Ser Gly Pro Ser Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met

165

170

175

Glu Gln Leu Glu Gly Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro

180

185

190

Arg Leu Pro Arg Gly Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu

195

200

205



Ile Thr Trp Ala Glu Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser  
 370 375 380

Asp Met Leu Ala Lys Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu  
 385 390 395 400

Leu Lys Ser Val Leu Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala  
 405 410 415

Val Val Ala Met Ile Gly Ser Val Glu Arg Phe Ile His His Val Asn  
 420 425 430

Ala Cys Met Arg Gln Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val  
 435 440 445

Ser Arg Ile Asp Ala Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val  
 450 455 460

Asp Lys Leu Leu Lys Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile  
 465 470 475 480

Pro Gly Ala Ser Pro Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser  
 485 490 495

Leu Arg Met Lys Glu Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe  
 500 505 510

Leu Phe Thr Asp Leu Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu  
 515 520 525

Arg Thr Arg Val Ile Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys  
 530 535 540

Arg Glu Leu Arg Asp Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu  
 545 550 555 560

Phe His Ser Ala Val Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala  
 565 570 575

Leu Cys Arg Gly Trp Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu  
 580 585 590

Gln Gln Leu Arg Ala Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln  
 595 600 605

Ser Leu Glu Glu Glu Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu  
 610 615 620

Glu Glu Glu Glu Glu Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser  
 625 630 635 640

Pro Thr Ile Met Arg Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys  
 645 650 655

Ala Ser Asp Gly Ser Thr Glu Thr Leu Ala Met Val Val Val Glu Pro  
 660 665 670

Gly Asp Thr Leu Ser Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser  
675 680 685

Gln Ser Asp Glu Thr Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro  
690 695 700

Thr Ser Glu Leu Leu Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser  
705 710 715 720

Met Asp Ser Ala Tyr Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe  
725 730 735

Val Ala Pro Gly Pro Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser  
740 745 750

Pro Arg Val Pro Ser Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr  
755 760 765

Pro Val Gln Leu Leu Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser  
770 775 780

Glu Ala Ser Leu Leu Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr  
785 790 795 800

Pro Ser Ala Pro Ser Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro  
805 810 815

Ala Pro Gly Ile Arg Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser  
585/735





agatgaagac cagggagagg aaaggtgga cctgaggecc ccatggagaa gggacgggca 60

ggatgtatgt caccagccg actgccagca gctgcaccgc cgggggcccc tcaacctctg 120

cgaggcctgt gacagcaagt tccacagcac c atg cat tat gat ggg cat gtc 172

Met His Tyr Asp Gly His Val

1

5

cgc ttc gac ctt ccc cca caa ggc tct gtg ctg gcc cgg aac gtg tcc 220

Arg Phe Asp Leu Pro Pro Gln Gly Ser Val Leu Ala Arg Asn Val Ser

10

15

20

acc cgg tca tgc ccg ccg cgc acc agc ccc gca gtg gac ttg gag gag 268

Thr Arg Ser Cys Pro Pro Arg Thr Ser Pro Ala Val Asp Leu Glu Glu

25

30

35

gag gag gag gag agc tct gtg gat ggc aaa ggg gac cgg aag agc aca 316

Glu Glu Glu Glu Ser Ser Val Asp Gly Lys Gly Asp Arg Lys Ser Thr

40

45

50

55

ggc ctg aaa ctc tcc aag aag aaa gca agg agg aga cac acg gat gac 364

Gly Leu Lys Leu Ser Lys Lys Lys Ala Arg Arg Arg His Thr Asp Asp

60

65

70

cca agc aag gaa tgc ttc act ctg aaa ttt gac ctg aat gtg gac att 412

Pro Ser Lys Glu Cys Phe Thr Leu Lys Phe Asp Leu Asn Val Asp Ile

75

80

85

gag aca gag atc gtc cca gcc atg aag aag aag tca ctg ggg gag gtg 460

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Glu Thr Glu Ile Val Pro Ala Met Lys Lys Lys Ser Leu Gly Glu Val  
 90 95 100

ctg ctg cct gta ttt gaa agg aag ggc att gcg ctg ggc aaa gtg gac 508  
 Leu Leu Pro Val Phe Glu Arg Lys Gly Ile Ala Leu Gly Lys Val Asp  
 105 110 115

atc tac ctg gac cag tcc aac aca ccc ctg tcc ctc acc ttc gag gcc 556  
 Ile Tyr Leu Asp Gln Ser Asn Thr Pro Leu Ser Leu Thr Phe Glu Ala  
 120 125 130 135

tac agg ttc ggg gga cac tac ctt cgt gtc aaa gcc cca gcc aag cct 604  
 Tyr Arg Phe Gly Gly His Tyr Leu Arg Val Lys Ala Pro Ala Lys Pro  
 140 145 150

gga gat gag ggc aag gtg gag cag ggc atg aag gac tcc aag tcc ctg 652  
 Gly Asp Glu Gly Lys Val Glu Gln Gly Met Lys Asp Ser Lys Ser Leu  
 155 160 165

agt ttg ccg att ctg cgg cca gct ggg acc ggg ccc ccc gcc ctg gag 700  
 Ser Leu Pro Ile Leu Arg Pro Ala Gly Thr Gly Pro Pro Ala Leu Glu  
 170 175 180

cgt gtg gac gcc cag agc cgc cgg gag agc ctg gac atc ttg gcc cct 748  
 Arg Val Asp Ala Gln Ser Arg Arg Glu Ser Leu Asp Ile Leu Ala Pro  
 185 190 195

ggc cgc cgc cgc aag aac atg tcg gag ttc ctg ggg gag gcg agc atc 796  
 Gly Arg Arg Arg Lys Asn Met Ser Glu Phe Leu Gly Glu Ala Ser Ile  
 588/735

... ..

1. The first step is to identify the key components of the system. This involves understanding the hardware, software, and data involved. For example, in a web application, this might include the server, the database, and the user interface.

1. 2. 3. 4. 5. 6. 7. 8. 9. 10. 11. 12. 13. 14. 15. 16. 17. 18. 19. 20. 21. 22. 23. 24. 25. 26. 27. 28. 29. 30. 31. 32. 33. 34. 35. 36. 37. 38. 39. 40. 41. 42. 43. 44. 45. 46. 47. 48. 49. 50. 51. 52. 53. 54. 55. 56. 57. 58. 59. 60. 61. 62. 63. 64. 65. 66. 67. 68. 69. 70. 71. 72. 73. 74. 75. 76. 77. 78. 79. 80. 81. 82. 83. 84. 85. 86. 87. 88. 89. 90. 91. 92. 93. 94. 95. 96. 97. 98. 99. 100. 101. 102. 103. 104. 105. 106. 107. 108. 109. 110. 111. 112. 113. 114. 115. 116. 117. 118. 119. 120. 121. 122. 123. 124. 125. 126. 127. 128. 129. 130. 131. 132. 133. 134. 135. 136. 137. 138. 139. 140. 141. 142. 143. 144. 145. 146. 147. 148. 149. 150. 151. 152. 153. 154. 155. 156. 157. 158. 159. 160. 161. 162. 163. 164. 165. 166. 167. 168. 169. 170. 171. 172. 173. 174. 175. 176. 177. 178. 179. 180. 181. 182. 183. 184. 185. 186. 187. 188. 189. 190. 191. 192. 193. 194. 195. 196. 197. 198. 199. 200. 201. 202. 203. 204. 205. 206. 207. 208. 209. 210. 211. 212. 213. 214. 215. 216. 217. 218. 219. 220. 221. 222. 223. 224. 225. 226. 227. 228. 229. 230. 231. 232. 233. 234. 235. 236. 237. 238. 239. 240. 241. 242. 243. 244. 245. 246. 247. 248. 249. 250. 251. 252. 253. 254. 255. 256. 257. 258. 259. 260. 261. 262. 263. 264. 265. 266. 267. 268. 269. 270. 271. 272. 273. 274. 275. 276. 277. 278. 279. 280. 281. 282. 283. 284. 285. 286. 287. 288. 289. 290. 291. 292. 293. 294. 295. 296. 297. 298. 299. 300. 301. 302. 303. 304. 305. 306. 307. 308. 309. 310. 311. 312. 313. 314. 315. 316. 317. 318. 319. 320. 321. 322. 323. 324. 325. 326. 327. 328. 329. 330. 331. 332. 333. 334. 335. 336. 337. 338. 339. 340. 341. 342. 343. 344. 345. 346. 347. 348. 349. 350. 351. 352. 353. 354. 355. 356. 357. 358. 359. 360. 361. 362. 363. 364. 365. 366. 367. 368. 369. 370. 371. 372. 373. 374. 375. 376. 377. 378. 379. 380. 381. 382. 383. 384. 385. 386. 387. 388. 389. 390. 391. 392. 393. 394. 395. 396. 397. 398. 399. 400. 401. 402. 403. 404. 405. 406. 407. 408. 409. 410. 411. 412. 413. 414. 415. 416. 417. 418. 419. 420. 421. 422. 423. 424. 425. 426. 427. 428. 429. 430. 431. 432. 433. 434. 435. 436. 437. 438. 439. 440. 441. 442. 443. 444. 445. 446. 447. 448. 449. 450. 451. 452. 453. 454. 455. 456. 457. 458. 459. 460. 461. 462. 463. 464. 465. 466. 467. 468. 469. 470. 471. 472. 473. 474. 475. 476. 477. 478. 479. 480. 481. 482. 483. 484. 485. 486. 487. 488. 489. 490. 491. 492. 493. 494. 495. 496. 497. 498. 499. 500. 501. 502. 503. 504. 505. 506. 507. 508. 509. 510. 511. 512. 513. 514. 515. 516. 517. 518. 519. 520. 521. 522. 523. 524. 525. 526. 527. 528. 529. 530. 531. 532. 533. 534. 535. 536. 537. 538. 539. 540. 541. 542. 543. 544. 545. 546. 547. 548. 549. 550. 551. 552. 553. 554. 555. 556. 557. 558. 559. 560. 561. 562. 563. 564. 565. 566. 567. 568. 569. 570. 571. 572. 573. 574. 575. 576. 577. 578. 579. 580. 581. 582. 583. 584. 585. 586. 587. 588. 589. 590. 591. 592. 593. 594. 595. 596. 597. 598. 599. 600. 601. 602. 603. 604. 605. 606. 607. 608. 609. 610. 611. 612. 613. 614. 615. 616. 617. 618. 619. 620. 621. 622. 623. 624. 625. 626. 627. 628. 629. 630. 631. 632. 633. 634. 635. 636. 637. 638. 639. 640. 641. 642. 643. 644. 645. 646. 647. 648. 649. 650. 651. 652. 653. 654. 655. 656. 657. 658. 659. 660. 661. 662. 663. 664. 665. 666. 667. 668. 669. 670. 671. 672. 673. 674. 675. 676. 677. 678. 679. 680. 681. 682. 683. 684. 685. 686. 687. 688. 689. 690. 691. 692. 693. 694. 695. 696. 697. 698. 699. 700. 701. 702. 703. 704. 705. 706. 707. 708. 709. 710. 711. 712. 713. 714. 715. 716. 717. 718. 719. 720. 721. 722. 723. 724. 725. 726. 727. 728. 729. 730. 731. 732. 733. 734. 735. 736. 737. 738. 739. 740. 741. 742. 743. 744. 745. 746. 747. 748. 749. 750. 751. 752. 753. 754. 755. 756. 757. 758. 759. 760. 761. 762. 763. 764. 765. 766. 767. 768. 769. 770. 771. 772. 773. 774. 775. 776. 777. 778. 779. 780. 781. 782. 783. 784. 785. 786. 787. 788. 789. 790. 791. 792. 793. 794. 795. 796. 797. 798. 799. 800. 801. 802. 803. 804. 805. 806. 807. 808. 809. 810. 811. 812. 813. 814. 815. 816. 817. 818. 819. 820. 821. 822. 823. 824. 825. 826. 827. 828. 829. 830. 831. 832. 833. 834. 835. 836. 837. 838. 839. 840.

gag aag ctg acc cgg cgg cag tgc cac cag cag gag gcg gtg tgg gag 1180  
Glu Lys Leu Thr Arg Arg Gln Cys His Gln Gln Glu Ala Val Trp Glu  
330 335 340

ctg ctg cac acg gag gcc tcc tac atc agg aaa ctg cgg gtg atc atc 1228  
Leu Leu His Thr Glu Ala Ser Tyr Ile Arg Lys Leu Arg Val Ile Ile  
345 350 355

aac ctg ttc ctg tgc tgc ctc ctg aac ctg caa gag tca ggg ctg ctg 1276  
Asn Leu Phe Leu Cys Cys Leu Leu Asn Leu Gln Glu Ser Gly Leu Leu  
360 365 370 375

tgt gag gtg gag gcg gag cgc ctg ttc agc aac atc ccg gag atc gcg 1324  
Cys Glu Val Glu Ala Glu Arg Leu Phe Ser Asn Ile Pro Glu Ile Ala  
380 385 390

cag ctg cac cgc agg ctg tgg gct agc gtg atg gcg ccg gtg ctg gag 1372  
Gln Leu His Arg Arg Leu Trp Ala Ser Val Met Ala Pro Val Leu Glu  
395 400 405

aag gcg cgg cgc acg cga gcg ctg cta cag ccc ggg gac ttc ctc aaa 1420  
Lys Ala Arg Arg Thr Arg Ala Leu Leu Gln Pro Gly Asp Phe Leu Lys  
410 415 420

ggc ttc aag atg ttc ggc tcg ctc ttc aag ccc tac atc cgc tac tgc 1468  
Gly Phe Lys Met Phe Gly Ser Leu Phe Lys Pro Tyr Ile Arg Tyr Cys  
425 430 435

Met Glu Glu Glu Gly Cys Met Glu Tyr Met Arg Gly Leu Leu Arg Asp  
440 445 450 455

aac gac ctc ttc cgg gcc tac atc acg tgg gcg gag aag cac cca cag 1564  
Asn Asp Leu Phe Arg Ala Tyr Ile Thr Trp Ala Glu Lys His Pro Gln  
460 465 470

tgc cag agg ctg aag ctg agc gac atg ctg gcc aaa ccc cac cag cgg 1612  
Cys Gln Arg Leu Lys Leu Ser Asp Met Leu Ala Lys Pro His Gln Arg  
475 480 485

ctc acc aag tac ccg ctg ctg ctc aag tcg gtg ctg agg aag acc gag 1660  
Leu Thr Lys Tyr Pro Leu Leu Leu Lys Ser Val Leu Arg Lys Thr Glu  
490 495 500

gag ccg cgc gcc aag gag gcc gtc gtc gcc atg atc ggc tcc gtg gag 1708  
Glu Pro Arg Ala Lys Glu Ala Val Val Ala Met Ile Gly Ser Val Glu  
505 510 515

cgc ttc atc cac cac gtg aac gcg tgc atg cgg cag cgg cag gag cgg 1756  
Arg Phe Ile His His Val Asn Ala Cys Met Arg Gln Arg Gln Glu Arg  
520 525 530 535

cag cgg ctg gcg gcc gtg gtg agc cgc atc gac gcc tac gag gtg gtg 1804  
Gln Arg Leu Ala Ala Val Val Ser Arg Ile Asp Ala Tyr Glu Val Val  
540 545 550

gaa agc agc agc gac gaa gtg gac aag ctc ctg aag gaa ttt ctg cac 1852  
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$$\frac{a_1}{a_2} = \frac{a_1 + a_2}{a_2} - 1 = \frac{a_1 + a_2}{a_2} - \frac{a_2}{a_2} = \frac{a_1 + a_2 - a_2}{a_2} = \frac{a_1}{a_2}$$

560

Leu Asp Leu Thr Ala Pro Ile Pro Gly Ala Ser Pro Glu Glu Thr Arg

575

Gln Leu Leu Leu Glu Gly Ser Leu Arg Met Lys Glu Gly Lys Asp Ser

590

Lys Met Asp Val Tyr Cys Phe Leu Phe Thr Asp Leu Leu Leu Val Thr

605

Lys Ala Val Lys Lys Ala Glu Arg Thr Arg Val Ile Arg Pro Pro Leu

625

Leu Val Asp Lys Ile Val Cys Arg Glu Leu Arg Asp Pro Gly Ser Phe

640

Leu Leu Ile Tyr Leu Asn Glu Phe His Ser Ala Val Gly Ala Tyr Thr

655

Phe Gln Ala Ser Gly Gln Ala Leu Cys Arg Gly Trp Val Asp Thr Ile

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act gcc tca tct gcc acg ccc acc agt gag ctg ctg ccc ctg ggt ccg 2572

Thr Ala Ser Ser Ala Thr Pro Thr Ser Glu Leu Leu Pro Leu Gly Pro

795

800

805

gtg gac ggc cgc tcc tgc tcc atg gac tct gcc tac ggc acc ctc tcc 2620

Val Asp Gly Arg Ser Cys Ser Met Asp Ser Ala Tyr Gly Thr Leu Ser

810

815

820

cca acc tcc tta caa gac ttt gtg gcc cca ggc cca atg gca gag cta 2668

Pro Thr Ser Leu Gln Asp Phe Val Ala Pro Gly Pro Met Ala Glu Leu

825

830

835

gtg cct cgg gcc cca gag tcc cca cga gtt cct tcc cct cca ccc tcg 2716

Val Pro Arg Ala Pro Glu Ser Pro Arg Val Pro Ser Pro Pro Pro Ser

840

845

850

855

ccc cgt ctc cgc cgc cgc acc cct gtc cag ctg ttg agc tgc ccg ccc 2764

Pro Arg Leu Arg Arg Arg Thr Pro Val Gln Leu Leu Ser Cys Pro Pro

860

865

870

cac ctg ctc aag tct aag tcc gag gcc agc ctc ctc cag ctg ctg gca 2812

His Leu Leu Lys Ser Lys Ser Glu Ala Ser Leu Leu Gln Leu Leu Ala

875

880

885

ggg gct ggc acc cat ggg aca ccc tct gcc ccc agc cgc agc ctg tca 2860

Gly Ala Gly Thr His Gly Thr Pro Ser Ala Pro Ser Arg Ser Leu Ser

890

895

900



gag ctc tgc ctg gct gtt cca gcc cca ggt att agg act cag ggc tcc 2908

Glu Leu Cys Leu Ala Val Pro Ala Pro Gly Ile Arg Thr Gln Gly Ser

905

910

915

cct cag gaa gct ggg ccc agc tgg gat tgc cga ggg gcc cct agc cct 2956

Pro Gln Glu Ala Gly Pro Ser Trp Asp Cys Arg Gly Ala Pro Ser Pro

920

925

930

935

ggc agc ggt cct ggg cta gtc ggc tgc ctg gcc ggg gaa cct gca ggc 3004

Gly Ser Gly Pro Gly Leu Val Gly Cys Leu Ala Gly Glu Pro Ala Gly

940

945

950

tcc cac agg aag agg tgt gga gac ctg ccc tcg ggg gcc tct ccc agg 3052

Ser His Arg Lys Arg Cys Gly Asp Leu Pro Ser Gly Ala Ser Pro Arg

955

960

965

gtc cag cct gag ccc cca cca ggg gtc tct gcc cag cac agg aag ctg 3100

Val Gln Pro Glu Pro Pro Pro Gly Val Ser Ala Gln His Arg Lys Leu

970

975

980

acc ctg gcc cag ctc tac cga atc agg acc acc ctg ctg ctt aac tcc 3148

Thr Leu Ala Gln Leu Tyr Arg Ile Arg Thr Thr Leu Leu Leu Asn Ser

985

990

995

acg ctc act gcc tcg gag gtc tgagcagagg gaggccccca agagtgccat 3199

Thr Leu Thr Ala Ser Glu Val

1000

1005

tgaccaagag acagcagaca gcctgcctcc tggggcgtgc cggcacctgc ttcagctact 3259

595/735



Lys Gly Asp Arg Lys Ser Thr Gly Leu Lys Leu Ser Lys Lys Lys Ala  
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Arg Arg Arg His Thr Asp Asp Pro Ser Lys Glu Cys Phe Thr Leu Lys  
65 70 75 80

Phe Asp Leu Asn Val Asp Ile Glu Thr Glu Ile Val Pro Ala Met Lys  
85 90 95

Lys Lys Ser Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg Lys Gly  
100 105 110

Ile Ala Leu Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn Thr Pro  
115 120 125

Leu Ser Leu Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr Leu Arg  
130 135 140

Val Lys Ala Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu Gln Gly  
145 150 155 160

Met Lys Asp Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro Ala Gly  
165 170 175

Thr Gly Pro Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg Arg Glu  
180 185 190

Ser Leu Asp Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met Ser Glu  
195 200 205

Phe Leu Gly Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr Pro Ser  
210 215 220

Ser Cys Ser Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr Gly Asp  
225 230 235 240

Ser Trp Lys Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe Ser Ser  
245 250 255

Gly Pro Ser Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met Glu Gln  
260 265 270

Leu Glu Gly Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro Arg Leu  
275 280 285

Pro Arg Gly Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu Tyr Asp  
290 295 300

Glu Asp Glu Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp Ser Trp  
305 310 315 320

Arg Glu Leu Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln Cys His  
325 330 335

Gln Gln Glu Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser Tyr Ile  
340 345 350

Arg Lys Leu Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu Leu Asn  
598/735

355 360 365

Leu Gln Glu Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg Leu Phe

370 375 380

Ser Asn Ile Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp Ala Ser

385 390 395 400

Val Met Ala Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala Leu Leu

405 410 415

Gln Pro Gly Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser Leu Phe

420 425 430

Lys Pro Tyr Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met Glu Tyr

435 440 445

Met Arg Gly Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr Ile Thr

450 455 460

Trp Ala Glu Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser Asp Met

465 470 475 480

Leu Ala Lys Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu Lys

485 490 495

Ser Val Leu Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala Val Val

500 505 510

Ala Met Ile Gly Ser Val Glu Arg Phe Ile His His Val Asn Ala Cys  
515 520 525

Met Arg Gln Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val Ser Arg  
530 535 540

Ile Asp Ala Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val Asp Lys  
545 550 555 560

Leu Leu Lys Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile Pro Gly  
565 570 575

Ala Ser Pro Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser Leu Arg  
580 585 590

Met Lys Glu Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe Leu Phe  
595 600 605

Thr Asp Leu Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu Arg Thr  
610 615 620

Arg Val Ile Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys Arg Glu  
625 630 635 640

Leu Arg Asp Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu Phe His  
645 650 655

Ser Ala Val Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala Leu Cys  
660 665 670

Arg Gly Trp Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu Gln Gln

675

680

685

Leu Arg Ala Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln Ser Leu

690

695

700

Glu Glu Glu Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu Glu Glu Glu

705

710

715

720

Glu Glu Glu Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser Pro Thr

725

730

735

Ile Met Arg Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys Ala Ser

740

745

750

Asp Gly Ser Thr Glu Thr Leu Ala Met Val Val Val Glu Pro Gly Asp

755

760

765

Thr Leu Ser Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser Gln Ser

770

775

780

Asp Glu Thr Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro Thr Ser

785

790

795

800

Glu Leu Leu Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser Met Asp

805

810

815

Ser Ala Tyr Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe Val Ala

601/735







Ser Leu Lys Ala Ala Arg Arg Ala Thr Gly Arg Pro Asp Arg Ser Arg  
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gca gcc ccg ccc aac atg gac cca gac ccc cag gcg ggc gtg cag gtg 257  
Ala Ala Pro Pro Asn Met Asp Pro Asp Pro Gln Ala Gly Val Gln Val  
40 45 50 55

ggc atg cgg gtg gtg cgc ggc gtg gac tgg aag tgg ggc cag cag gac 305  
Gly Met Arg Val Val Arg Gly Val Asp Trp Lys Trp Gly Gln Gln Asp  
60 65 70

ggc ggc gag ggc ggc gtg ggc acg gtg gtg gag ctt ggc cgc cac ggc 353  
Gly Gly Glu Gly Gly Val Gly Thr Val Val Glu Leu Gly Arg His Gly  
75 80 85

agc ccc tcg aca ccc gac cgc aca gtg gtc gtg cag tgg gac cag ggc 401  
Ser Pro Ser Thr Pro Asp Arg Thr Val Val Val Gln Trp Asp Gln Gly  
90 95 100

acg cgc acc aac tac cgc gcc ggc tac cag ggc gcg cac gac ctg ctg 449  
Thr Arg Thr Asn Tyr Arg Ala Gly Tyr Gln Gly Ala His Asp Leu Leu  
105 110 115

ctg tac gac aac gcc cag atc ggc gtc cgg cac ccc aac atc atc tgt 497  
Leu Tyr Asp Asn Ala Gln Ile Gly Val Arg His Pro Asn Ile Ile Cys  
120 125 130 135

gac tgc tgc aag aag cac ggg ctg cgg ggg atg cgc tgg aag tgc cgt 545  
Asp Cys Cys Lys Lys His Gly Leu Arg Gly Met Arg Trp Lys Cys Arg





gac gtg gtc cgg gtc atc ggc gac ctt gac aca gtg aag cgg ctg cag 1265

Asp Val Val Arg Val Ile Gly Asp Leu Asp Thr Val Lys Arg Leu Gln

380

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390

gct ggg cat ggc gag tgg acg gac gac atg gcc cct gcc ctg ggc cgc . 1313

Ala Gly His Gly Glu Trp Thr Asp Asp Met Ala Pro Ala Leu Gly Arg

395

400

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gtc ggg aag gtg gtg aaa gtg ttt gga gac ggg aac ctg cgt gta gca 1361

Val Gly Lys Val Val Lys Val Phe Gly Asp Gly Asn Leu Arg Val Ala

410

415

420

gtc gct ggt cag cgg tgg acc ttc agc ccc tcc tgc ctg gtg gcc tac 1409

Val Ala Gly Gln Arg Trp Thr Phe Ser Pro Ser Cys Leu Val Ala Tyr

425

430

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cgg ccc gag gag gat gcc aac ctg gac gtg gcc gag cgc gcc cgg gag 1457

Arg Pro Glu Glu Asp Ala Asn Leu Asp Val Ala Glu Arg Ala Arg Glu

440

445

450

455

aac aaa agc tca ctg agc gtg gcc ctg gac aag ctt cgg gcc cag aag 1505

Asn Lys Ser Ser Leu Ser Val Ala Leu Asp Lys Leu Arg Ala Gln Lys

460

465

470

agt gac cca gag cac ccg gga agg ctg gtg gtg gag gtg gcc ctg ggt 1553

Ser Asp Pro Glu His Pro Gly Arg Leu Val Val Glu Val Ala Leu Gly

475

480

485

aac gca gcc cgg gct ctg gac ctg ctg cgg agg cgc cca gag caa gtg 1601



600 605 610 615

atc tcg gcg ggc act gga gcc agc ggc att gtc gag gtc ctc acg gag 1985  
Ile Ser Ala Gly Thr Gly Ala Ser Gly Ile Val Glu Val Leu Thr Glu

620 625 630

gtg cca aac atc gat gtt acc gcc acc aac agc cag ggt ttc acc ctg 2033  
Val Pro Asn Ile Asp Val Thr Ala Thr Asn Ser Gln Gly Phe Thr Leu

635 640 645

ctg cac cat gcc tcc ctc aag ggt cac gcg cta gct gtg aga aag att 2081  
Leu His His Ala Ser Leu Lys Gly His Ala Leu Ala Val Arg Lys Ile

650 655 660

ctg gct cgg gcg cgg cag ctg gtg gac gcc aag aag gag gac ggc ttc 2129  
Leu Ala Arg Ala Arg Gln Leu Val Asp Ala Lys Lys Glu Asp Gly Phe

665 670 675

acg gcg ctg cat ctg gct gcc ctc aac aac cac cgc gag gtg gcc cag 2177  
Thr Ala Leu His Leu Ala Ala Leu Asn Asn His Arg Glu Val Ala Gln

680 685 690 695

atc ctc atc cgg gag ggc cgc tgt gac gtg aac gtg cgc aac cgg aag 2225  
Ile Leu Ile Arg Glu Gly Arg Cys Asp Val Asn Val Arg Asn Arg Lys

700 705 710

ctg cag tcc ccg ctg cat ctc gcc gtg caa cag gcc cac gtg ggg ctg 2273  
Leu Gln Ser Pro Leu His Leu Ala Val Gln Gln Ala His Val Gly Leu

715 720 725

gtg ccg cta ctg gtg gac gct ggg tgc agt gtc aac gcc gag gac gag 2321  
Val Pro Leu Leu Val Asp Ala Gly Cys Ser Val Asn Ala Glu Asp Glu  
730 735 740

gag ggg gac aca gcc ctg cac gtg gcg ctg cag cgt cat cag ctg ctg 2369  
Glu Gly Asp Thr Ala Leu His Val Ala Leu Gln Arg His Gln Leu Leu  
745 750 755

ccc ctg gtg gct gat ggg gcc ggg ggg gac cca ggg ccc ttg cag ctg 2417  
Pro Leu Val Ala Asp Gly Ala Gly Gly Asp Pro Gly Pro Leu Gln Leu  
760 765 770 775

ctg tcc agg cta cag gcc teg ggc ctc ccc ggc agc gcg gag ctg acg 2465  
Leu Ser Arg Leu Gln Ala Ser Gly Leu Pro Gly Ser Ala Glu Leu Thr  
780 785 790

gtg ggc gcg gcg gtc gcc tgc ttc ctg gcg ctg gag ggc gcc gac gtg 2513  
Val Gly Ala Ala Val Ala Cys Phe Leu Ala Leu Glu Gly Ala Asp Val  
795 800 805

agc tac acc aac cac cgc ggt cgg agc ccg ctg gac ctg gcc gcc gag 2561  
Ser Tyr Thr Asn His Arg Gly Arg Ser Pro Leu Asp Leu Ala Ala Glu  
810 815 820

ggt cgc gtg ctc aag gcc ctt cag ggc tgc gcc cag cgc ttc cgg gag 2609  
Gly Arg Val Leu Lys Ala Leu Gln Gly Cys Ala Gln Arg Phe Arg Glu  
825 830 835



cgg cag gcg ggc ggg ggc gcg gcc ccg ggc ccc agg caa acg ctc ggg 2657

Arg Gln Ala Gly Gly Gly Ala Ala Pro Gly Pro Arg Gln Thr Leu Gly

840 845 850 855

acc ccc aac acc gtg acg aac ctg cac gtg ggc gcc gcg ccg ggg ccc 2705

Thr Pro Asn Thr Val Thr Asn Leu His Val Gly Ala Ala Pro Gly Pro

860 865 870

gag gcc gct gag tgc ctg gtg tgc tcc gag ctg gcg ctg ctg gtg ctg 2753

Glu Ala Ala Glu Cys Leu Val Cys Ser Glu Leu Ala Leu Leu Val Leu

875 880 885

ttc tcg ccg tgc cag cac cgc acc gtg tgt gag gag tgc gcg cgc agg 2801

Phe Ser Pro Cys Gln His Arg Thr Val Cys Glu Glu Cys Ala Arg Arg

890 895 900

atg aag aag tgc atc agg tgc cag gtg gtc gtc agc aag aaa ctg cgc 2849

Met Lys Lys Cys Ile Arg Cys Gln Val Val Val Ser Lys Lys Leu Arg

905 910 915

cca gac ggc tct gag gtg gcg agc gcc gcc ccc gcc ccc ggc ccg ccg 2897

Pro Asp Gly Ser Glu Val Ala Ser Ala Ala Pro Ala Pro Gly Pro Pro

920 925 930 935

cgc cag ctg gtg gag gag ctg cag agc cgc tac cgg cag atg gag gaa 2945

Arg Gln Leu Val Glu Glu Leu Gln Ser Arg Tyr Arg Gln Met Glu Glu

940 945 950

cgc atc acc tgc ccc atc tgc atc gac agg cac atc cgc ctc gtg ttc 2993

Arg Ile Thr Cys Pro Ile Cys Ile Asp Arg His Ile Arg Leu Val Phe  
955 960 965

cag tgc ggc cac ggc gca tgc gcc ccc tgc ggc tcc gcg ctc agc gcc 3041  
Gln Cys Gly His Gly Ala Cys Ala Pro Cys Gly Ser Ala Leu Ser Ala  
970 975 980

tgc ccc atc tgc cgc cag ccc atc cgc gac cgc atc cag atc ttc gtg 3089  
Cys Pro Ile Cys Arg Gln Pro Ile Arg Asp Arg Ile Gln Ile Phe Val  
985 990 995

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aaaagaaaga ttctcgat 3168

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- <211> 999
- <212> PRT
- <213> Homo sapiens

<400> 160  
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Ala Ser Gly Leu Gln Pro Arg Ser Leu Lys Ala Ala Arg Arg Ala Thr  
20 25 30

Gly Arg Pro Asp Arg Ser Arg Ala Ala Pro Pro Asn Met Asp Pro Asp  
612/735

35 40 45

Pro Gln Ala Gly Val Gln Val Gly Met Arg Val Val Arg Gly Val Asp  
50 55 60

Trp Lys Trp Gly Gln Gln Asp Gly Gly Glu Gly Gly Val Gly Thr Val  
65 70 75 80

Val Glu Leu Gly Arg His Gly Ser Pro Ser Thr Pro Asp Arg Thr Val  
85 90 95

Val Val Gln Trp Asp Gln Gly Thr Arg Thr Asn Tyr Arg Ala Gly Tyr  
100 105 110

Gln Gly Ala His Asp Leu Leu Leu Tyr Asp Asn Ala Gln Ile Gly Val  
115 120 125

Arg His Pro Asn Ile Ile Cys Asp Cys Cys Lys Lys His Gly Leu Arg  
130 135 140

Gly Met Arg Trp Lys Cys Arg Val Cys Leu Asp Tyr Asp Leu Cys Thr  
145 150 155 160

Gln Cys Tyr Met His Asn Lys His Glu Leu Ala His Ala Phe Asp Arg  
165 170 175

Tyr Glu Thr Ala His Ser Arg Pro Val Thr Leu Ser Pro Arg Gln Gly  
180 185 190

Leu Pro Arg Ile Pro Leu Arg Gly Ile Phe Gln Gly Ala Lys Val Val  
 195 200 205

Arg Gly Pro Phe Trp Glu Trp Gly Ser Gln Asp Gly Gly Glu Gly Lys  
 210 215 220

Pro Gly Arg Val Val Asp Ile Arg Gly Trp Asp Val Glu Thr Gly Arg  
 225 230 235 240

Ser Val Ala Ser Val Thr Trp Ala Asp Gly Thr Thr Asn Val Tyr Arg  
 245 250 255

Val Gly His Lys Gly Lys Val Asp Leu Lys Cys Val Gly Glu Ala Ala  
 260 265 270

Gly Gly Phe Tyr Tyr Lys Asp His Leu Pro Arg Leu Gly Lys Pro Ala  
 275 280 285

Glu Leu Gln Arg Arg Val Ser Ala Asp Ser Gln Pro Phe Gln His Gly  
 290 295 300

Asp Lys Val Lys Cys Leu Leu Asp Thr Asp Val Leu Arg Glu Met Gln  
 305 310 315 320

Glu Gly His Gly Gly Trp Asn Pro Arg Met Ala Glu Phe Ile Gly Gln  
 325 330 335

Thr Gly Thr Val His Arg Ile Thr Asp Arg Gly Asp Val Arg Val Gln  
 340 345 350

Phe Asn His Glu Thr Arg Trp Thr Phe His Pro Gly Ala Leu Thr Lys  
355 360 365

His His Ser Phe Trp Val Gly Asp Val Val Arg Val Ile Gly Asp Leu  
370 375 380

Asp Thr Val Lys Arg Leu Gln Ala Gly His Gly Glu Trp Thr Asp Asp  
385 390 395 400

Met Ala Pro Ala Leu Gly Arg Val Gly Lys Val Val Lys Val Phe Gly  
405 410 415

Asp Gly Asn Leu Arg Val Ala Val Ala Gly Gln Arg Trp Thr Phe Ser  
420 425 430

Pro Ser Cys Leu Val Ala Tyr Arg Pro Glu Glu Asp Ala Asn Leu Asp  
435 440 445

Val Ala Glu Arg Ala Arg Glu Asn Lys Ser Ser Leu Ser Val Ala Leu  
450 455 460

Asp Lys Leu Arg Ala Gln Lys Ser Asp Pro Glu His Pro Gly Arg Leu  
465 470 475 480

Val Val Glu Val Ala Leu Gly Asn Ala Ala Arg Ala Leu Asp Leu Leu  
485 490 495

Arg Arg Arg Pro Glu Gln Val Asp Thr Lys Asn Gln Gly Arg Thr Ala  
615/735

500

505

510

Leu Gln Val Ala Ala Tyr Leu Gly Gln Val Glu Leu Ile Arg Leu Leu  
515 520 525

Leu Gln Ala Arg Ala Gly Val Asp Leu Pro Asp Asp Glu Gly Asn Thr  
530 535 540

Ala Leu His Tyr Ala Ala Leu Gly Asn Gln Pro Glu Ala Thr Arg Val  
545 550 555 560

Leu Leu Ser Ala Gly Cys Arg Ala Asp Ala Ile Asn Ser Thr Gln Ser  
565 570 575

Thr Ala Leu His Val Ala Val Gln Arg Gly Phe Leu Glu Val Val Arg  
580 585 590

Ala Leu Cys Glu Arg Gly Cys Asp Val Asn Leu Pro Asp Ala His Ser  
595 600 605

Asp Thr Pro Leu His Ser Ala Ile Ser Ala Gly Thr Gly Ala Ser Gly  
610 615 620

Ile Val Glu Val Leu Thr Glu Val Pro Asn Ile Asp Val Thr Ala Thr  
625 630 635 640

Asn Ser Gln Gly Phe Thr Leu Leu His His Ala Ser Leu Lys Gly His  
645 650 655

Ala Leu Ala Val Arg Lys Ile Leu Ala Arg Ala Arg Gln Leu Val Asp  
660 665 670

Ala Lys Lys Glu Asp Gly Phe Thr Ala Leu His Leu Ala Ala Leu Asn  
675 680 685

Asn His Arg Glu Val Ala Gln Ile Leu Ile Arg Glu Gly Arg Cys Asp  
690 695 700

Val Asn Val Arg Asn Arg Lys Leu Gln Ser Pro Leu His Leu Ala Val  
705 710 715 720

Gln Gln Ala His Val Gly Leu Val Pro Leu Leu Val Asp Ala Gly Cys  
725 730 735

Ser Val Asn Ala Glu Asp Glu Glu Gly Asp Thr Ala Leu His Val Ala  
740 745 750

Leu Gln Arg His Gln Leu Leu Pro Leu Val Ala Asp Gly Ala Gly Gly  
755 760 765

Asp Pro Gly Pro Leu Gln Leu Leu Ser Arg Leu Gln Ala Ser Gly Leu  
770 775 780

Pro Gly Ser Ala Glu Leu Thr Val Gly Ala Ala Val Ala Cys Phe Leu  
785 790 795 800

Ala Leu Glu Gly Ala Asp Val Ser Tyr Thr Asn His Arg Gly Arg Ser  
805 810 815

Pro Leu Asp Leu Ala Ala Glu Gly Arg Val Leu Lys Ala Leu Gln Gly

820

825

830

Cys Ala Gln Arg Phe Arg Glu Arg Gln Ala Gly Gly Gly Ala Ala Pro

835

840

845

Gly Pro Arg Gln Thr Leu Gly Thr Pro Asn Thr Val Thr Asn Leu His

850

855

860

Val Gly Ala Ala Pro Gly Pro Glu Ala Ala Glu Cys Leu Val Cys Ser

865

870

875

880

Glu Leu Ala Leu Leu Val Leu Phe Ser Pro Cys Gln His Arg Thr Val

885

890

895

Cys Glu Glu Cys Ala Arg Arg Met Lys Lys Cys Ile Arg Cys Gln Val

900

905

910

Val Val Ser Lys Lys Leu Arg Pro Asp Gly Ser Glu Val Ala Ser Ala

915

920

925

Ala Pro Ala Pro Gly Pro Pro Arg Gln Leu Val Glu Glu Leu Gln Ser

930

935

940

Arg Tyr Arg Gln Met Glu Glu Arg Ile Thr Cys Pro Ile Cys Ile Asp

945

950

955

960

Arg His Ile Arg Leu Val Phe Gln Cys Gly His Gly Ala Cys Ala Pro



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980

985

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Asp Arg Ile Gln Ile Phe Val

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cactggcgcg atgcgggccc tcctctcggc tg atg ggt tgg aag ccc agc gag 113

Met Gly Trp Lys Pro Ser Glu

1

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gct aga ggc cag tcc caa agt ctc cag gca tca ggg ctg cag ccc agg 161

Ala Arg Gly Gln Ser Gln Ser Leu Gln Ala Ser Gly Leu Gln Pro Arg

10

15

20



gac tgc tgc aag aag cac ggg ctg cgg ggg atg cgc tgg aag tgc cgt 545

Asp Cys Cys Lys Lys His Gly Leu Arg Gly Met Arg Trp Lys Cys Arg

140

145

150

gtg tgc ctg gac tac gac ctc tgc acg cag tgc tac atg cac aac aag 593

Val Cys Leu Asp Tyr Asp Leu Cys Thr Gln Cys Tyr Met His Asn Lys

155

160

165

cat gag ctc gcc cac gcc ttc gac cgc tac gag acc gct cac tcg cgc 641

His Glu Leu Ala His Ala Phe Asp Arg Tyr Glu Thr Ala His Ser Arg

170

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Pro Val Thr Leu Ser Pro Arg Gln Gly Leu Pro Arg Ile Pro Leu Arg

185

190

195

ggc atc ttc cag gga gcg aag gtg gtg cga ggc ccc ttc tgg gag tgg 737

Gly Ile Phe Gln Gly Ala Lys Val Val Arg Gly Pro Phe Trp Glu Trp

200

205

210

215

ggc tca cag gat gga ggg gaa ggg aaa ccg ggc cgt gtg gtg gac atc 785

Gly Ser Gln Asp Gly Gly Glu Gly Lys Pro Gly Arg Val Val Asp Ile

220

225

230

cgt ggc tgg gat gtg gag aca ggc cgg agt gtg gcc agc gtg acg tgg 833

Arg Gly Trp Asp Val Glu Thr Gly Arg Ser Val Ala Ser Val Thr Trp

235

240

245

gct gat ggt acc acc aat gtg tac cgt gtg ggc cac aag ggc aag gtg 881

Ala Asp Gly Thr Thr Asn Val Tyr Arg Val Gly His Lys Gly Lys Val  
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gac ctc aag tgt gtg ggc gag gca gcg ggc ggc ttc tac tac aag gac 929  
Asp Leu Lys Cys Val Gly Glu Ala Ala Gly Gly Phe Tyr Tyr Lys Asp  
265 270 275

cac ctc cca agg ctc ggc aag ccg gcg gag ctg cag cgc agg gtg agt 977  
His Leu Pro Arg Leu Gly Lys Pro Ala Glu Leu Gln Arg Arg Val Ser  
280 285 290 295

gct gac agc cag ccc ttc cag cac ggg gac aag gtc aag tgt ctg ctg 1025  
Ala Asp Ser Gln Pro Phe Gln His Gly Asp Lys Val Lys Cys Leu Leu  
300 305 310

gac act gat gtc ctg cgg gag atg cag gaa ggc cac ggc ggc tgg aac 1073  
Asp Thr Asp Val Leu Arg Glu Met Gln Glu Gly His Gly Gly Trp Asn  
315 320 325

ccc agg atg gcg gag ttt atc gga cag acg ggc acc gtg cat cgt atc 1121  
Pro Arg Met Ala Glu Phe Ile Gly Gln Thr Gly Thr Val His Arg Ile  
330 335 340

acg gac cgc ggg gac gtg cgc gtg cag ttc aac cac gag acg cgc tgg 1169  
Thr Asp Arg Gly Asp Val Arg Val Gln Phe Asn His Glu Thr Arg Trp  
345 350 355

acc ttc cac ccc ggg gcg ctc acc aag cac cac tcc ttc tgg gtg ggc 1217  
Thr Phe His Pro Gly Ala Leu Thr Lys His His Ser Phe Trp Val Gly  
622/735



aac gca gcc cgg gct ctg gac ctg ctg cgg agg cgc cca gag caa gtg 1601  
Asn Ala Ala Arg Ala Leu Asp Leu Leu Arg Arg Arg Pro Glu Gln Val  
490 495 500

gac acc aag aac caa ggc agg acc gct ctg caa gtg gct gcc tac ctg 1649  
Asp Thr Lys Asn Gln Gly Arg Thr Ala Leu Gln Val Ala Ala Tyr Leu  
505 510 515

ggc cag gtg gag ttg ata cgg ctg ctg cta caa gcc agg gcg ggc gtg 1697  
Gly Gln Val Glu Leu Ile Arg Leu Leu Leu Gln Ala Arg Ala Gly Val  
520 525 530 535

gac ctg ccg gac gac gag ggc aac acg gca ctg cac tac gcg gcc ctg 1745  
Asp Leu Pro Asp Asp Glu Gly Asn Thr Ala Leu His Tyr Ala Ala Leu  
540 545 550

ggg aac cag ccc gag gcc acc agg gtg ctc ctg agt gct ggg tgc cgg 1793  
Gly Asn Gln Pro Glu Ala Thr Arg Val Leu Leu Ser Ala Gly Cys Arg  
555 560 565

gcg gac gcc atc aac agc acc cag agc aca gca ctg cac gtg gcc gtg 1841  
Ala Asp Ala Ile Asn Ser Thr Gln Ser Thr Ala Leu His Val Ala Val  
570 575 580

cag agg ggc ttc ctg gag gtg gtg cgg gcc ctg tgt gag cgc ggc tgt 1889  
Gln Arg Gly Phe Leu Glu Val Val Arg Ala Leu Cys Glu Arg Gly Cys  
585 590 595









cgc atc acc tgc ccc atc tgc atc gac agc cac atc cgc ctc gtg ttc 2993  
Arg Ile Thr Cys Pro Ile Cys Ile Asp Ser His Ile Arg Leu Val Phe  
955 960 965

cag tgc ggc cac ggc gca tgc gcc ccc tgc ggc tcc gcg ctc agc gcc 3041  
Gln Cys Gly His Gly Ala Cys Ala Pro Cys Gly Ser Ala Leu Ser Ala  
970 975 980

tgc ccc atc tgc cgc cag ccc atc cgc gac cgc atc cag atc ttc gtg 3089  
Cys Pro Ile Cys Arg Gln Pro Ile Arg Asp Arg Ile Gln Ile Phe Val  
985 990 995

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aaaagaaaga ttctcgat 3168

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Ala Ser Gly Leu Gln Pro Arg Ser Leu Lys Ala Ala Arg Arg Ala Thr  
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Gly Arg Pro Asp Arg Ser Arg Ala Ala Pro Pro Asn Met Asp Pro Asp  
 35 40 45

Pro Gln Ala Gly Val Gln Val Gly Met Arg Val Val Arg Gly Val Asp  
 50 55 60

Trp Lys Trp Gly Gln Gln Asp Gly Gly Glu Gly Gly Val Gly Thr Val  
 65 70 75 80

Val Glu Leu Gly Arg His Gly Ser Pro Ser Thr Pro Asp Arg Thr Val  
 85 90 95

Val Val Gln Trp Asp Gln Gly Thr Arg Thr Asn Tyr Arg Ala Gly Tyr  
 100 105 110

Gln Gly Ala His Asp Leu Leu Leu Tyr Asp Asn Ala Gln Ile Gly Val  
 115 120 125

Arg His Pro Asn Ile Ile Cys Asp Cys Cys Lys Lys His Gly Leu Arg  
 130 135 140

Gly Met Arg Trp Lys Cys Arg Val Cys Leu Asp Tyr Asp Leu Cys Thr  
 145 150 155 160

Gln Cys Tyr Met His Asn Lys His Glu Leu Ala His Ala Phe Asp Arg  
 165 170 175

Tyr Glu Thr Ala His Ser Arg Pro Val Thr Leu Ser Pro Arg Gln Gly  
 629/735



Thr Gly Thr Val His Arg Ile Thr Asp Arg Gly Asp Val Arg Val Gln  
 340 345 350

Phe Asn His Glu Thr Arg Trp Thr Phe His Pro Gly Ala Leu Thr Lys  
 355 360 365

His His Ser Phe Trp Val Gly Asp Val Val Arg Val Ile Gly Asp Leu  
 370 375 380

Asp Thr Val Lys Arg Leu Gln Ala Gly His Gly Glu Trp Thr Asp Asp  
 385 390 395 400

Met Ala Pro Ala Leu Gly Arg Val Gly Lys Val Val Lys Val Phe Gly  
 405 410 415

Asp Gly Asn Leu Arg Val Ala Val Ala Gly Gln Arg Trp Thr Phe Ser  
 420 425 430

Pro Ser Cys Leu Val Ala Tyr Arg Pro Glu Glu Asp Ala Asn Leu Asp  
 435 440 445

Val Ala Glu Arg Ala Arg Glu Asn Lys Ser Ser Leu Ser Val Ala Leu  
 450 455 460

Asp Lys Leu Arg Ala Gln Lys Ser Asp Pro Glu His Pro Gly Arg Leu  
 465 470 475 480

Val Val Glu Val Ala Leu Gly Asn Ala Ala Arg Ala Leu Asp Leu Leu  
 485 490 495





Ala Leu Glu Gly Ala Asp Val Ser Tyr Thr Asn His Arg Gly Arg Ser  
805 810 815

Pro Leu Asp Leu Ala Ala Glu Gly Arg Val Leu Lys Ala Leu Gln Gly  
820 825 830

Cys Ala Gln Arg Phe Arg Glu Arg Gln Ala Gly Gly Gly Ala Ala Pro  
835 840 845

Gly Pro Arg Gln Thr Leu Gly Thr Pro Asn Thr Val Thr Asn Leu His  
850 855 860

Val Gly Ala Ala Pro Gly Pro Glu Ala Ala Glu Cys Leu Val Cys Ser  
865 870 875 880

Glu Leu Ala Leu Leu Val Leu Phe Ser Pro Cys Gln His Arg Thr Val  
885 890 895

Cys Glu Glu Cys Ala Arg Arg Met Lys Lys Cys Ile Arg Cys Gln Val  
900 905 910

Val Val Ser Lys Lys Leu Arg Pro Asp Gly Ser Glu Val Ala Ser Ala  
915 920 925

Ala Pro Ala Pro Gly Pro Pro Arg Gln Leu Val Glu Glu Leu Gln Ser  
930 935 940

Arg Tyr Arg Gln Met Glu Glu Arg Ile Thr Cys Pro Ile Cys Ile Asp  
945 950 955 960



Ser His Ile Arg Leu Val Phe Gln Cys Gly His Gly Ala Cys Ala Pro  
965 970 975

Cys Gly Ser Ala Leu Ser Ala Cys Pro Ile Cys Arg Gln Pro Ile Arg  
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Asp Arg Ile Gln Ile Phe Val  
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<213> Mus musculus

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Met Ile Ala Trp Arg Leu Pro Leu

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tgc gtg ctc ttg gtg gcc tcc gtc gag agc cac ctg ggg gcc ctg ggg 162

Cys Val Leu Leu Val Ala Ser Val Glu Ser His Leu Gly Ala Leu Gly  
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ccc aag aac gtc tcg cag aaa gac gcg gag ttt gag cgc acc tac gcg 210  
 Pro Lys Asn Val Ser Gln Lys Asp Ala Glu Phe Glu Arg Thr Tyr Ala  
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gac gac gtc aac agc gag ctg gtc aac atc tac acc ttc aac cac acc 258  
 Asp Asp Val Asn Ser Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr  
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gtg acc cgc aac cgg acc gag ggt gtg cga gtg tct gtg aat gtc ctg 306  
 Val Thr Arg Asn Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu  
 60 65 70

aac aag cag aaa ggg gcg cct ttg ctg ttc gtg gtc cgc cag aag gag 354  
 Asn Lys Gln Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu  
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gct gtt gtg tcc ttc cag gtg ccc cta atc ctt cga gga ctg tat cag 402  
 Ala Val Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Leu Tyr Gln  
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cgg aag tac ctc tac caa aaa gtg gaa cga act ctg tgt cag ccc ccc 450  
 Arg Lys Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro  
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 Thr Lys Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser Thr







Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val Gln Leu  
 475 480 485

gtg atc acc tac cag acg gtg gtg aat gtc aca ggg aac cag gac atc 1602  
 Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile  
 490 495 500

tgc tac tac aac ttc ctc tgt gcc cac ccg ctg ggc aac ctc agc gcc 1650  
 Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly Asn Leu Ser Ala  
 505 510 515 520

ttc aac aac atc ctc agc aac ttg ggg tac atc ctg ctg ggg ctg ctc 1698  
 Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile Leu Leu Gly Leu Leu  
 525 530 535

ttc ctg ctc atc atc ctg cag cga gag atc aat cat aac cgg gcc ctg 1746  
 Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile Asn His Asn Arg Ala Leu  
 540 545 550

ctg cgg aat gac ctc tat gct ctg gag tgt ggg atc ccc aaa cac ttt 1794  
 Leu Arg Asn Asp Leu Tyr Ala Leu Glu Cys Gly Ile Pro Lys His Phe  
 555 560 565

ggt ctg ttt tac gcc atg ggc aca gca ctg atg atg gag ggg cta ctt 1842  
 Gly Leu Phe Tyr Ala Met Gly Thr Ala Leu Met Met Glu Gly Leu Leu  
 570 575 580

agt gcc tgt tac cac gtc tgc ccc aac tac acc aac ttc cag ttt gat 1890  
 Ser Ala Cys Tyr His Val Cys Pro Asn Tyr Thr Asn Phe Gln Phe Asp  
 640/735



ctg gtc atg ggc aac att atc aac tgg tgc ctg gct gca tac gga ctc 2274

Leu Val Met Gly Asn Ile Ile Asn Trp Ser Leu Ala Ala Tyr Gly Leu

715

720

725

atc atg cgc ccc aat gac ttt gct tcc tac ttg ctg gca att ggc atc 2322

Ile Met Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala Ile Gly Ile

730

735

740

tgc aac ctg ctg ctt tat ttc gcc ttc tac atc atc atg aag ctc cgg 2370

Cys Asn Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile Met Lys Leu Arg

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750

755

760

agc ggc gag agg atc aag ctc atc cct ctg ctt tgc atc gtc tgc acc 2418

Ser Gly Glu Arg Ile Lys Leu Ile Pro Leu Leu Cys Ile Val Cys Thr

765

770

775

tcc gtg gtc tgg ggc ttc gcg ctc ttc ttc ttc ttc cag gga ctg agc 2466

Ser Val Val Trp Gly Phe Ala Leu Phe Phe Phe Phe Gln Gly Leu Ser

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785

790

acg tgg cag aaa acc ccc gca gag tcc agg gag cac aac cgc gac tgc 2514

Thr Trp Gln Lys Thr Pro Ala Glu Ser Arg Glu His Asn Arg Asp Cys

795

800

805

atc ctc ctc gac ttc ttt gat gac cac gat atc tgg cac ttc ctg tcc 2562

Ile Leu Leu Asp Phe Phe Asp Asp His Asp Ile Trp His Phe Leu Ser

810

815

820



tcc att gcc atg ttt ggg tcc ttc ctg gtt ttg ctg acg ttg gat gac 2610  
 Ser Ile Ala Met Phe Gly Ser Phe Leu Val Leu Leu Thr Leu Asp Asp  
 825 830 835 840

gac ttg gac aca gta cag cgg gac aag atc tat gtc ttc tagcagcatc 2659  
 Asp Leu Asp Thr Val Gln Arg Asp Lys Ile Tyr Val Phe  
 845 850

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acaagaacac caagggtgtg agtcccagct ctgctgcccc gcattggatg tcgtggcaag 2779

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actggctctc catttgtecc ttggagagg aaggtgggaa ggcaatgtcc tgtcccattt 3019

catgccttgc attctgcccc tcccttccct cctctcagct taggacacac agccctttct 3079

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cagatgcagg taggagactt tgggggctgg ccagctgggtg ccaggctttc ggtgctaagg 3259

cctggaaggg gcctaggtac gaccctcctc cctgacctgt gcttggagct ggctcttcag 3319













|   |     |         |
|---|-----|---------|
| 755   | 760 | 765     |
| Pro Leu Leu Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu |     |         |
| 770   | 775 | 780     |
| Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu |     |         |
| 785   | 790 | 795 800 |
| Ser Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp |     |         |
| 805   | 810 | 815     |
| His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser Phe |     |         |
| 820   | 825 | 830     |
| Leu Val Leu Leu Thr Leu Asp Asp Asp Leu Asp Thr Val Gln Arg Asp |     |         |
| 835   | 840 | 845     |
| Lys Ile Tyr Val Phe   |     |         |
| 850   |     |         |

<210> 165

<211> 3138

<212> DNA

<213> Homo sapiens

<220>

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Ile Asp Arg Ala Cys Pro Glu Ser Gly His Pro Arg Val Leu Ala Asp

335 340 345

tct ttt cct ggc agt tcc cct tat gag ggt tac aac tat ggc tcc ttt 1169  
Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe

350 355 360

gag aat gtt tct gga tct acc gat ggt ctg gtt gac agc gct ggc act 1217  
Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser Ala Gly Thr

365 370 375

ggg gac ctc tct tac ggt tac cag ggg cac gac cag ttc aag cgg cgc 1265  
Gly Asp Leu Ser Tyr Gly Tyr Gln Gly His Asp Gln Phe Lys Arg Arg

380 385 390

ctc ccc tct ggc cag atg cgg cag ctg tgc att gcc atg ggc cgc tcc 1313  
Leu Pro Ser Gly Gln Met Arg Gln Leu Cys Ile Ala Met Gly Arg Ser

395 400 405 410

ttt gaa cct gta ggt act cgg ccc cga gtg gac tcc atg agc tct gtg 1361  
Phe Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val

415 420 425

gag gag gat gac tac gac aca ttg acc gac atc gat tcc gac aag aat 1409  
Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn

430 435 440

gtc att cgc acc aag caa tac ctc tat gtg gct gac ctg gca cgg aag 1457  
 Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala Arg Lys  
 445 450 455

gac aag cgt gtt ctg cgg aaa aag tac cag atc tac ttc tgg aac att 1505  
 Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile  
 460 465 470

gcc acc att gct gtc ttc tat gcc ctt cct gtg gtg cag ctg gtg atc 1553  
 Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val Gln Leu Val Ile  
 475 480 485 490

acc tac cag acg gtg gtg aat gtc aca ggg aat cag gac atc tgc tac 1601  
 Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr  
 495 500 505

tac aac ttc ctc tgc gcc cac cca ctg ggc aat ctc agc gcc ttc aac 1649  
 Tyr Asn Phe Leu Cys Ala His Pro Leu Gly Asn Leu Ser Ala Phe Asn  
 510 515 520

aac atc ctc agc aac ctg ggg tac atc ctg ctg ggg ctg ctt ttc ctg 1697  
 Asn Ile Leu Ser Asn Leu Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu  
 525 530 535

ctc atc atc ctg caa cgg gag atc aac cac aac cgg gcc ctg ctg cgc 1745  
 Leu Ile Ile Leu Gln Arg Glu Ile Asn His Asn Arg Ala Leu Leu Arg  
 540 545 550



Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp

670

675

680

tcg ggg atc ttc cgc cgc atc ctc cac gtg ctc tac aca gac tgc atc 2177

Ser Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp Cys Ile

685

690

695

cgg cag tgc agc ggg ccg ctc tac gtg gac cgc atg gtg ctg ctg gtc 2225

Arg Gln Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val Leu Leu Val

700

705

710

atg ggc aac gtc atc aac tgg tcg ctg gct gcc tat ggg ctt atc atg 2273

Met Gly Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met

715

720

725

730

cgc ccc aat gat ttc gct tcc tac ttg ttg gcc att ggc atc tgc aac 2321

Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn

735

740

745

ctg ctc ctt tac ttc gcc ttc tac atc atc atg aag ctc cgg agt ggg 2369

Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly

750

755

760

gag agg atc aag ctc atc ccc ctg ctc tgc atc gtt tgc acc tcc gtg 2417

Glu Arg Ile Lys Leu Ile Pro Leu Leu Cys Ile Val Cys Thr Ser Val

765

770

775

gtc tgg ggc ttc gcg ctc ttc ttc ttc ttc cag gga ctc agc acc tgg 2465

Val Trp Gly Phe Ala Leu Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp

657/735







Leu Ile Leu Arg Gly Met Phe Gln Arg Lys Tyr Leu Tyr Gln Lys Val  
100 105 110

Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys Asn Glu Ser Glu Ile Gln  
115 120 125

Phe Phe Tyr Val Asp Val Ser Thr Leu Ser Pro Val Asn Thr Thr Tyr  
130 135 140

Gln Leu Arg Val Ser Arg Met Asp Asp Phe Val Leu Arg Thr Gly Glu  
145 150 155 160

Gln Phe Ser Phe Asn Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr  
165 170 175

Glu Phe Pro Glu Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Asn  
180 185 190

Lys Ala Phe Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro  
195 200 205

Val Tyr Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met Tyr Gln Thr  
210 215 220

Met Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser  
225 230 235 240

Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala Cys  
660/735



Arg Gln Leu Cys Ile Ala Met Gly Arg Ser Phe Glu Pro Val Gly Thr  
405 410 415

Arg Pro Arg Val Asp Ser Met Ser Ser Val Glu Glu Asp Asp Tyr Asp  
420 425 430

Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn Val Ile Arg Thr Lys Gln  
435 440 445

Tyr Leu Tyr Val Ala Asp Leu Ala Arg Lys Asp Lys Arg Val Leu Arg  
450 455 460

Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile Ala Thr Ile Ala Val Phe  
465 470 475 480

Tyr Ala Leu Pro Val Val Gln Leu Val Ile Thr Tyr Gln Thr Val Val  
485 490 495

Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala  
500 505 510

His Pro Leu Gly Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu  
515 520 525

Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg  
530 535 540

Glu Ile Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu  
545 550 555 560

Glu Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr  
 565 570 575

Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys Pro  
 580 585 590

Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met Ile Ala  
 595 600 605

Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro Asp Ile Asn  
 610 615 620

Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile Val Ile Phe Phe  
 625 630 635 640

Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn Thr Ala Phe Trp Ile  
 645 650 655

Val Phe Ser Ile Ile His Ile Ile Ala Thr Leu Leu Leu Ser Thr Gln  
 660 665 670

Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp Ser Gly Ile Phe Arg Arg  
 675 680 685

Ile Leu His Val Leu Tyr Thr Asp Cys Ile Arg Gln Cys Ser Gly Pro  
 690 695 700

Leu Tyr Val Asp Arg Met Val Leu Leu Val Met Gly Asn Val Ile Asn  
 663/735

705                      710                      715                      720

Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met Arg Pro Asn Asp Phe Ala  
725 730 735

Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala  
740 745 750

Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile  
755 760 765

Pro Leu Leu Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu  
770 775 780

Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu  
785 790 795 800

Ser Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp  
805 810 815

His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser Phe  
820 825 830

Leu Val Ser Gly Pro Pro Gly Arg Ala Gly Trp Val Arg Glu Gly Ser  
835 840 845

Ser Cys Leu Leu Pro Cys Gly  
850 855



Cys Cys Val Arg Ala Leu Ser Ile Gln Arg Leu Trp Tyr Phe Trp Phe  
50 55 60 65

ctt ctg atg atg ggc gtg ctt ttc tgc tgc gga gcc ggc ttc ttc atc 298  
Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe Ile  
70 75 80

cgg agg cgc atg tac ccc ccg ccg ctg atc gag gag cca gcc ttc aat 346  
Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe Asn  
85 90 95

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Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn Pro  
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Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser Pro  
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Gln Gly Ser Val Ala Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr Pro  
150 155 160

ccg ccc ccg tac gaa cag gta gtg aag gcc aag tagtggggtg cccacgtgca 591  
Pro Pro Pro Tyr Glu Gln Val Val Lys Ala Lys



165

170

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gggc 2815

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<211> 172

<212> PRT

<213> Homo sapiens

<400> 168

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12323 12324 12325

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12323 12324 12325

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12323 12324 12325

670/735

165

170

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<222> (136).. (1755)

<400> 169

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agaatctgag cagca atg ccg ttt gct gaa gac aag acc tat aag tat atc 171

Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile

1 5 10

tgc cgc aat ttc agc aat ttt tgc aat gtg gat gtt gta gag att ctg 219

Cys Arg Asn Phe Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu

15 20 25

cct tac ctg ccc tgc ctc aca gca aga gac cag gat cga ctg cgg gcc 267

Pro Tyr Leu Pro Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala

30 35 40

acc tgc aca ctc tca ggg aac cgg gac acc ctc tgg cat ctc ttc aat 315

Thr Cys Thr Leu Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn  
45 50 55 60

acc ctt cag cgg cgg ccc ggc tgg gtg gag tac ttc att gcg gca ctg 363

Thr Leu Gln Arg Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu  
65 70 75

agg ggc tgt gag cta gtt gat ctc gcg gac gaa gtg gcc tct gtc tac 411

Arg Gly Cys Glu Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr  
80 85 90

cag agc tac cag cct cgg acc tcg gac cgt ccc cca gac cca ctg gag 459

Gln Ser Tyr Gln Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu  
95 100 105

cca ccg tca ctt cct gct gag agg cca ggg ccc ccc aca cct gct gcg 507

Pro Pro Ser Leu Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala  
110 115 120

gcc cac agc atc ccc tac aac agc tgc aga gag aag gag cca agt tac 555

Ala His Ser Ile Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr  
125 130 135 140

ccc atg cct gtc cag gag acc cag gcg cca gag tcc cca gga gag aat 603

Pro Met Pro Val Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn  
145 150 155

tca gag caa gcc ctg cag acg ctc agc ccc aga gcc atc cca agg aat 651

Ser Glu Gln Ala Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn

160

165

170

cca gat ggt ggc ccc ctg gag tcc tcc tct gac ctg gca gcc ctc agc 699

Pro Asp Gly Gly Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser

175

180

185

cct ctg acc tcc agc ggg cat cag gag cag gac aca gaa ctg ggc agt 747

Pro Leu Thr Ser Ser Gly His Gln Glu Gln Asp Thr Glu Leu Gly Ser

190

195

200

acc cac aca gca ggt gcg acc tcc agc ctc aca cca tcc cgt ggg cct 795

Thr His Thr Ala Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro

205

210

215

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gtg tct cca tct gtc tcc ttc cag ccc ctg gcc cgt tcc acc ccc agg 843

Val Ser Pro Ser Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg

225

230

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gca agc cgc ttg cct gga ccc aca ggg tca gtt gta tct act ggc acc 891

Ala Ser Arg Leu Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr

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tcc ttc tcc tcc tca tcc cct ggc ttg gcc tct gca ggg gct gca gag 939

Ser Phe Ser Ser Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu

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ggt aaa cag ggt gca gag agt gac cag gcc gag cct atc atc tgc tcc 987





385

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ggc ctt ggg tcg gag ctg agt aag cct ggc gtg ctg gca tcc cag gta 1419  
Gly Leu Gly Ser Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val  
415 420 425

gac agc ccg ttc tcg ggc tgc ttc gag gat ctt gcc atc agt gcc agc 1467  
Asp Ser Pro Phe Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser  
430 435 440

acc tcc ttg ggc atg ggg ccc tgc cat ggc cca gag gag aat gag tat 1515  
Thr Ser Leu Gly Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr  
445 450 455 460

aag tcc gag ggc acc ttt ggg atc cac gtg gct gag aac ccc agc atc 1563  
Lys Ser Glu Gly Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile  
465 470 475

cag ctc ctg gag ggc aac cct ggg cca cct gcg gac ccg gat ggc ggc 1611  
Gln Leu Leu Glu Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly  
480 485 490

ccc agg cca caa gcc gac cgg aag ttc cag gag agg gag gtg cca tgc 1659  
Pro Arg Pro Gln Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys  
495 500 505



tggcatttac caagggttgg atatatgtta ttatcactat taagtgttga ggggccaggc 2415

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atcccatcc cccaccacca atcttaaaaa gcctctgtc cccctacct aaacccagc 3255

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<212> PRT

<213> Homo sapiens

<400> 170

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Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu

35 40 45

Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr Leu Gln Arg

50 55 60

Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu Arg Gly Cys Glu

65 70 75 80

Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr Gln Ser Tyr Gln

85 90 95

Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu Pro Pro Ser Leu  
 100 105 110

Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala Ala His Ser Ile  
 115 120 125

Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr Pro Met Pro Val  
 130 135 140

Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn Ser Glu Gln Ala  
 145 150 155 160

Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn Pro Asp Gly Gly  
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Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser Pro Leu Thr Ser  
 180 185 190

Ser Gly His Gln Glu Gln Asp Thr Glu Leu Gly Ser Thr His Thr Ala  
 195 200 205

Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro Val Ser Pro Ser  
 210 215 220

Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg Ala Ser Arg Leu  
 225 230 235 240

Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr Ser Phe Ser Ser  
 679/735



Ser Ser Ala Trp Leu Asp Ser Ser Ser Glu Asn Arg Gly Leu Gly Ser  
405 410 415

Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val Asp Ser Pro Phe  
420 425 430

Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser Thr Ser Leu Gly  
435 440 445

Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr Lys Ser Glu Gly  
450 455 460

Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile Gln Leu Leu Glu  
465 470 475 480

Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly Pro Arg Pro Gln  
485 490 495

Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys His Arg Pro Ser  
500 505 510

Pro Gly Ala Leu Trp Leu Gln Val Ala Val Thr Gly Val Leu Val Val  
515 520 525

Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His  
530 535 540

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DATE 01-29-2001 BY 60322 UCBAW



〈221〉 CDS

<400> 171

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gggaaggagg cagggcaagg ccgggcttgg gggcaggtgg tccgggcata cagccttgaa 240

g atg cac aag agg aaa gga ccc ccg gga ccc ccg ggc aga ggc gcc gcg 289

Met His Lys Arg Lys Gly Pro Pro Gly Pro Pro Gly Arg Gly Ala Ala

1

5

10

15

gcc gcc cgc cag ctg ggc ctg ctg gtt gac ctc tcc cca gat ggc ctg 337

Ala Ala Arg Gln Leu Gly Leu Leu Val Asp Leu Ser Pro Asp Gly Leu

20

25

30

atg atc cct gag gac ggg gct aac gat gaa gaa ctg gag gct gag ttc 385

Met Ile Pro Glu Asp Gly Ala Asn Asp Glu Glu Leu Glu Ala Glu Phe

35

40

45









385                      390                      395                      400

gct gaa ttg ccc gtg ccc cca ggc ttc ccc cca atc cag ggc ctg gag 1489  
Ala Glu Leu Pro Val Pro Pro Gly Phe Pro Pro Ile Gln Gly Leu Glu  
405 410 415

gcc acc aag ccc acc cag cag agt ctg gtg ggt gtc ctg gag act gcc 1537  
Ala Thr Lys Pro Thr Gln Gln Ser Leu Val Gly Val Leu Glu Thr Ala  
420 425 430

atg aag ctg gcc aac cag gat gaa ggc cca gag gat gaa gag gat gag 1585  
Met Lys Leu Ala Asn Gln Asp Glu Gly Pro Glu Asp Glu Glu Asp Glu  
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gtg cct aag aag cag aac agc cct gtg gcc ccc aca gcc cag ccc aaa 1633  
Val Pro Lys Lys Gln Asn Ser Pro Val Ala Pro Thr Ala Gln Pro Lys  
450 455 460

gcc cca ccc tca aga act ccc cag tcg gga tca gcc cca aca gcc aaa 1681  
Ala Pro Pro Ser Arg Thr Pro Gln Ser Gly Ser Ala Pro Thr Ala Lys  
465 470 475 480

gcg ccc ccc aaa gcc aca tcc acc aga gcc cag cag cag ctg gcc ttc 1729  
Ala Pro Pro Lys Ala Thr Ser Thr Arg Ala Gln Gln Gln Leu Ala Phe  
485 490 495

cta gag ggc cgc aag aag cag ctc ctg cag gcc gca ctg cga gcc aag 1777  
Leu Glu Gly Arg Lys Lys Gln Leu Leu Gln Ala Ala Leu Arg Ala Lys  
500 505 510

cag aaa aac gac gtg gag ggt gcc aag atg cac ctg cgc caa gcc aag 1825

Gln Lys Asn Asp Val Glu Gly Ala Lys Met His Leu Arg Gln Ala Lys

515

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525

gga ctg gag cct atg ctg gag gcc tcg cgc aat ggg ctg cct gtg gac 1873

Gly Leu Glu Pro Met Leu Glu Ala Ser Arg Asn Gly Leu Pro Val Asp

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540

atc acc aag gtg ccg cct gcc cct gtc aac aag gac gac ttt gcc ctg 1921

Ile Thr Lys Val Pro Pro Ala Pro Val Asn Lys Asp Asp Phe Ala Leu

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550

555

560

gtc cag cgg cct ggc ccg ggt ctg tct cag gag gcc gcc cgg cgc tat 1969

Val Gln Arg Pro Gly Pro Gly Leu Ser Gln Glu Ala Ala Arg Arg Tyr

565

570

575

ggt gaa ctc acc aag ctc ata cgg cag cag cac gag atg tgc ctg aac 2017

Gly Glu Leu Thr Lys Leu Ile Arg Gln Gln His Glu Met Cys Leu Asn

580

585

590

cac tca aac caa ttc acc cag ctg ggc aac atc act gaa acc acc aag 2065

His Ser Asn Gln Phe Thr Gln Leu Gly Asn Ile Thr Glu Thr Thr Lys

595

600

605

ttt gaa aag ttg gcg gag gac tgt aag cgg agc atg gac att ctg aag 2113

Phe Glu Lys Leu Ala Glu Asp Cys Lys Arg Ser Met Asp Ile Leu Lys

610

615

620

caa gcc ttc gtc cgg ggt ctc ccc acg ccc acc gcc cgc ttt gag caa 2161

Gln Ala Phe Val Arg Gly Leu Pro Thr Pro Thr Ala Arg Phe Glu Gln

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agg acc ttc agc gtc atc aag atc ttc cct gac ctc agc agc aac gac 2209

Arg Thr Phe Ser Val Ile Lys Ile Phe Pro Asp Leu Ser Ser Asn Asp

645 650 655

atg ctc ctc ttc atc gtg aag ggc atc aac ttg ccc aca ccc cca gga 2257

Met Leu Leu Phe Ile Val Lys Gly Ile Asn Leu Pro Thr Pro Pro Gly

660 665 670

ctg tcc cct ggc gat ctg gat gtc ttt gtt cgg ttt gac ttc ccc tat 2305

Leu Ser Pro Gly Asp Leu Asp Val Phe Val Arg Phe Asp Phe Pro Tyr

675 680 685

ccc aac gtg gaa gaa gct cag aaa gac aag acc agt gtg atc aag aac 2353

Pro Asn Val Glu Glu Ala Gln Lys Asp Lys Thr Ser Val Ile Lys Asn

690 695 700

aca gac tcc cct gag ttc aag gag cag ttc aaa ctc tgc atc aac cgc 2401

Thr Asp Ser Pro Glu Phe Lys Glu Gln Phe Lys Leu Cys Ile Asn Arg

705 710 715 720

agc cac cgt ggc ttc cga agg gcc atc cag acc aag ggc atc aag ttc 2449

Ser His Arg Gly Phe Arg Arg Ala Ile Gln Thr Lys Gly Ile Lys Phe

725 730 735

gaa gtg gtt cac aag ggg ggg ctg ttc aag act gac cgg gtg ctg ggg 2497

688/735



850

855

860

ctc agg cag gcg cgg cgg ccg gtg ccc cca gaa gtg gcc cag cag tac 2881

Leu Arg Gln Ala Arg Arg Pro Val Pro Pro Glu Val Ala Gln Gln Tyr

865

870

875

880

cag gac atc atg caa cgc agc cag tgg cag agg gca cag ctg gag cag 2929

Gln Asp Ile Met Gln Arg Ser Gln Trp Gln Arg Ala Gln Leu Glu Gln

885

890

895

ggg ggt gtg ggc atc cga cgg gaa tac aca gcc cag ctg gag cgg cag 2977

Gly Gly Val Gly Ile Arg Arg Glu Tyr Thr Ala Gln Leu Glu Arg Gln

900

905

910

ctg cag ttc tac acg gag gct gcc cgg cgc ctg ggc aac gat ggc agc 3025

Leu Gln Phe Tyr Thr Glu Ala Ala Arg Arg Leu Gly Asn Asp Gly Ser

915

920

925

agg gat gct gca aag gag gcg ctc tat agg cgg aat ctg gta ggg agt 3073

Arg Asp Ala Ala Lys Glu Ala Leu Tyr Arg Arg Asn Leu Val Gly Ser

930

935

940

gag ctg cag cgg ctc cgc agg tgaggagccc atggggcgagg cagccccag 3124

Glu Leu Gln Arg Leu Arg Arg

945

950

aaagcgggca gcaggccccg ataccgggaa gagccgacac agccacgaac cagacaagca 3184

gacaatcagc ggacaatcgg ttctggactc acccctcacc cgggccccca gccccgccag 3244









355 360 365

Lys Gly Asp Gln Arg Lys Ala Arg Met His Glu Arg Ile Val Lys Gln  
370 375 380

Tyr Gln Asp Ala Ile Arg Ala His Lys Ala Gly Arg Ala Val Asp Val  
385 390 395 400

Ala Glu Leu Pro Val Pro Pro Gly Phe Pro Pro Ile Gln Gly Leu Glu  
405 410 415

Ala Thr Lys Pro Thr Gln Gln Ser Leu Val Gly Val Leu Glu Thr Ala  
420 425 430

Met Lys Leu Ala Asn Gln Asp Glu Gly Pro Glu Asp Glu Glu Asp Glu  
435 440 445

Val Pro Lys Lys Gln Asn Ser Pro Val Ala Pro Thr Ala Gln Pro Lys  
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Ala Pro Pro Ser Arg Thr Pro Gln Ser Gly Ser Ala Pro Thr Ala Lys  
465 470 475 480

Ala Pro Pro Lys Ala Thr Ser Thr Arg Ala Gln Gln Gln Leu Ala Phe  
485 490 495

Leu Glu Gly Arg Lys Lys Gln Leu Leu Gln Ala Ala Leu Arg Ala Lys  
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Gln Lys Asn Asp Val Glu Gly Ala Lys Met His Leu Arg Gln Ala Lys  
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Gly Leu Glu Pro Met Leu Glu Ala Ser Arg Asn Gly Leu Pro Val Asp  
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Ile Thr Lys Val Pro Pro Ala Pro Val Asn Lys Asp Asp Phe Ala Leu  
545 550 555 560

Val Gln Arg Pro Gly Pro Gly Leu Ser Gln Glu Ala Ala Arg Arg Tyr  
565 570 575

Gly Glu Leu Thr Lys Leu Ile Arg Gln Gln His Glu Met Cys Leu Asn  
580 585 590

His Ser Asn Gln Phe Thr Gln Leu Gly Asn Ile Thr Glu Thr Thr Lys  
595 600 605

Phe Glu Lys Leu Ala Glu Asp Cys Lys Arg Ser Met Asp Ile Leu Lys  
610 615 620

Gln Ala Phe Val Arg Gly Leu Pro Thr Pro Thr Ala Arg Phe Glu Gln  
625 630 635 640

Arg Thr Phe Ser Val Ile Lys Ile Phe Pro Asp Leu Ser Ser Asn Asp  
645 650 655

Met Leu Leu Phe Ile Val Lys Gly Ile Asn Leu Pro Thr Pro Pro Gly  
660 665 670  
695/735

Leu Ser Pro Gly Asp Leu Asp Val Phe Val Arg Phe Asp Phe Pro Tyr  
675 680 685

Pro Asn Val Glu Glu Ala Gln Lys Asp Lys Thr Ser Val Ile Lys Asn  
690 695 700

Thr Asp Ser Pro Glu Phe Lys Glu Gln Phe Lys Leu Cys Ile Asn Arg  
705 710 715 720

Ser His Arg Gly Phe Arg Arg Ala Ile Gln Thr Lys Gly Ile Lys Phe  
725 730 735

Glu Val Val His Lys Gly Gly Leu Phe Lys Thr Asp Arg Val Leu Gly  
740 745 750

Thr Ala Gln Leu Lys Leu Asp Ala Leu Glu Ile Ala Cys Glu Val Arg  
755 760 765

Glu Ile Leu Glu Val Leu Asp Gly Arg Arg Pro Thr Gly Gly Arg Leu  
770 775 780

Glu Val Met Val Arg Ile Arg Glu Pro Leu Thr Ala Gln Gln Leu Glu  
785 790 795 800

Thr Thr Thr Glu Arg Trp Leu Val Ile Asp Pro Val Pro Ala Ala Val  
805 810 815

Pro Thr Gln Val Ala Gly Pro Lys Gly Lys Ala Pro Pro Val Pro Ala  
696/735

820

825

830

Pro Ala Arg Glu Ser Gly Asn Arg Ser Ala Arg Pro Leu His Ser Leu

835

840

845

Ser Val Leu Ala Phe Asp Gln Glu Arg Leu Glu Arg Lys Ile Leu Ala

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855

860

Leu Arg Gln Ala Arg Arg Pro Val Pro Pro Glu Val Ala Gln Gln Tyr

865

870

875

880

Gln Asp Ile Met Gln Arg Ser Gln Trp Gln Arg Ala Gln Leu Glu Gln

885

890

895

Gly Gly Val Gly Ile Arg Arg Glu Tyr Thr Ala Gln Leu Glu Arg Gln

900

905

910

Leu Gln Phe Tyr Thr Glu Ala Ala Arg Arg Leu Gly Asn Asp Gly Ser

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Arg Asp Ala Ala Lys Glu Ala Leu Tyr Arg Arg Asn Leu Val Gly Ser

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Glu Leu Gln Arg Leu Arg Arg

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<400> 173

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gcacctagca ggctctctgg gaaaaaaaaa tcc atg ggt gac aga aga ttt att 594

Met Gly Asp Arg Arg Phe Ile



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Asp Phe Gln Phe Gln Asp Leu Asn Ser Ser Leu Arg Pro Arg Leu Gly

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20

aat gca act gcc aat aat act tgc att gtt gat gat tcc ttc aag tat 690

Asn Ala Thr Ala Asn Asn Thr Cys Ile Val Asp Asp Ser Phe Lys Tyr

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aat ttg aat ggt gct gtc tat agt gtt gta ttc atc ctg ggt cta ata 738

Asn Leu Asn Gly Ala Val Tyr Ser Val Val Phe Ile Leu Gly Leu Ile

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Ser Glu Thr Ala Thr Phe Ile Thr Asn Leu Ala Leu Ser Asp Leu Leu

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Phe Val Cys Thr Leu Pro Phe Lys Ile Phe Tyr Asn Phe Asn Arg His

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Trp Pro Phe Gly Asp Thr Leu Cys Lys Ile Ser Gly Thr Ala Phe Leu

105

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115



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235 240 245

ttg aag atg atc aca gtg cat atg gca gtg ttt gtg gta tgc ttt gta 1362  
Leu Lys Met Ile Thr Val His Met Ala Val Phe Val Val Cys Phe Val  
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cca tac aac tcc gtt ctc ttt tta tat gcc ttg gta cgc tcc caa gcc 1410  
Pro Tyr Asn Ser Val Leu Phe Leu Tyr Ala Leu Val Arg Ser Gln Ala  
265 270 275

att act aat tgc tta ttg gaa agg ttt gca aag atc atg tac cca att 1458  
Ile Thr Asn Cys Leu Leu Glu Arg Phe Ala Lys Ile Met Tyr Pro Ile  
280 285 290 295

acc ttg tgc ctt gca act ctg aat tgt tgc ttt gat cct ttt atc tat 1506  
Thr Leu Cys Leu Ala Thr Leu Asn Cys Cys Phe Asp Pro Phe Ile Tyr  
300 305 310

tac ttc act ctt gaa tcc ttt cag aag tcc ttt tat atc aat aca cat 1554  
Tyr Phe Thr Leu Glu Ser Phe Gln Lys Ser Phe Tyr Ile Asn Thr His  
315 320 325

ata agg atg gag tcg ctg ttt aag act gag aca cct ctg acc ccc aaa 1602  
Ile Arg Met Glu Ser Leu Phe Lys Thr Glu Thr Pro Leu Thr Pro Lys  
330 335 340

cct tcc ctt cca gct atc caa gag gaa gtt agt gat caa aca aca aat 1650  
701/735

Pro Ser Leu Pro Ala Ile Gln Glu Glu Val Ser Asp Gln Thr Thr Asn

345 350 355

aat ggt ggt gaa tta atg ctg gaa tcc acc ttc taggtaccag aattgtcttt 1703

Asn Gly Gly Glu Leu Met Leu Glu Ser Thr Phe

360 365 370

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Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Thr Phe Ile Thr Asn  
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Leu Ala Leu Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe Lys Ile  
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Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu Cys Lys  
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Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe  
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Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val Cys Ala  
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Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser Leu Phe  
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Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu Gly Phe  
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Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile Phe Ile  
195 200 205

Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser Cys Ser  
210 215 220

Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser Gln Ile  
225 230 235 240

Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His Met Ala  
245 250 255

Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe Leu Tyr  
260 265 270

Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Leu Leu Glu Arg Phe  
275 280 285

Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu Asn Cys  
290 295 300

Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe Gln Lys  
305 310 315 320

Ser Phe Tyr Ile Asn Thr His Ile Arg Met Glu Ser Leu Phe Lys Thr  
325 330 335

Glu Thr Pro Leu Thr Pro Lys Pro Ser Leu Pro Ala Ile Gln Glu Glu  
705/735











ctataatttt tcctatgcta taaactaaag atttgaagct aatgatactg agaataatgc 1276

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gcttggttgg aatttcattg tategcatta tccaggtggc tagtggcatt tgataatata 1456

gagatgactt tgaaactttc aaaaaggtat ttctattcca atgatatttg gtaattaggt 1516

tgggcctata aatatagaac aaattcaggg atttttaaaa aattgtgtta ctactgatat 1576

atgctagttt tattttattt ttttggactg tcattgagtt tatttttagca caagaatatt 1636

tttagcctaa cattattaat aagaaatgtg tcaaattttt aacattggta aaatatgtta 1696

tgtgcatttt gaaaacagaa acaaattgc gttggcatgt acgtgggtgg gaagaaaaag 1756

aaaattaaca ggatttacac aattataatc accagcagtg tgagttttaa aaacttcgtt 1816

gtttttacac caaattaaaa ttttcatgtc aaacttcaaa gccagaaagc tgctaaatac 1876

gtgtctggca ggtaaaagct ggaaaattac ttaaaacagg aaagtgtcaa taaaaaaact 1936

tgagcaacac caacatattt tttcttaaaa tgtcacgtta tcttcatttt gggaaactag 1996

gttctataaa atatttatcc tccctgttat actttggagc acagcacagc cagaaagggg 2056

ctgcatttgt gccaggtca ggagcaaatt gaaaaaaaa ataaagtaat actaaaaaat 2116

caaactataa acccaaaaca tttattaaaa cctgaattaa tccttttttg aggaggagt 2176

agagatatat aacctgaaaa tacttattct ttcttatcga attttggagc ctaatatagc 2236

caggagctgc tgaatttgtg cccttgatt ggaaccaaataaaaaaaaaa aaaaaaaatt 2296

cct 2299

<210> 176

<211> 370

<212> PRT

<213> Homo sapiens

<400> 176

Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Ser Asn Ser

1 5 10 15

Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr Cys Ile

20 25 30

Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr Ser Val

35 40 45

Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Val Ser Leu Phe Val Phe

50 55 60

Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Ile Phe Ile Thr Asn  
65 70 75 80

Leu Ala Val Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe Lys Ile  
85 90 95

Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu Cys Lys  
100 105 110

Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met Leu Phe  
115 120 125

Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe  
130 135 140

Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val Cys Ala  
145 150 155 160

Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser Leu Phe  
165 170 175

Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu Gly Phe  
180 185 190

Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile Phe Ile  
195 200 205

Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser Cys Ser  
712/735

210

215

220

Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser Gln Ile

225

230

235

240

Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His Met Ala

245

250

255

Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe Leu Tyr

260

265

270

Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Phe Leu Glu Arg Phe

275

280

285

Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu Asn Cys

290

295

300

Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe Gln Lys

305

310

315

320

Ser Phe Tyr Ile Asn Ala His Ile Arg Met Glu Ser Leu Phe Lys Thr

325

330

335

Glu Thr Pro Leu Thr Thr Lys Pro Ser Leu Pro Ala Ile Gln Glu Glu

340

345

350

Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu Glu Ser

355

360

365

Thr Phe  
370

<210> 177  
<211> 973  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (30).. (416)

<400> 177

cagacagcgg cgggcgcagg acgtgcact atg gct cgg ggc tcg ctg cgc cgg 53  
Met Ala Arg Gly Ser Leu Arg Arg

1 5

ttg ctg cgg ctc ctc gtg ctg ggg ctc tgg ctg gcg ttg ctg cgc tcc 101  
Leu Leu Arg Leu Leu Val Leu Gly Leu Trp Leu Ala Leu Leu Arg Ser

10 15 20

gtg gcc ggg gag caa gcg cca ggc acc gcc ccc tgc tcc cgc ggc agc 149  
Val Ala Gly Glu Gln Ala Pro Gly Thr Ala Pro Cys Ser Arg Gly Ser

25 30 35 40

tcc tgg agc gcg gac ctg gac aag tgc atg gac tgc gcg tct tgc agg 197  
Ser Trp Ser Ala Asp Leu Asp Lys Cys Met Asp Cys Ala Ser Cys Arg



45

50

55

gcg cga ccg cac agc gac ttc tgc ctg ggc tgc gct gca gca cct cct 245

Ala Arg Pro His Ser Asp Phe Cys Leu Gly Cys Ala Ala Ala Pro Pro

60

65

70

gcc ccc ttc cgg ctg ctt tgg ccc atc ctt ggg ggc gct ctg agc ctg 293

Ala Pro Phe Arg Leu Leu Trp Pro Ile Leu Gly Gly Ala Leu Ser Leu

75

80

85

acc ttc gtg ctg ggg ctg ctt tct ggc ttt ttg gtc tgg aga cga tgc 341

Thr Phe Val Leu Gly Leu Leu Ser Gly Phe Leu Val Trp Arg Arg Cys

90

95

100

cgc agg aga gag aag ttc acc acc ccc ata gag gag acc ggc gga gag 389

Arg Arg Arg Glu Lys Phe Thr Thr Pro Ile Glu Glu Thr Gly Gly Glu

105

110

115

120

ggc tgc cca gct gtg gcg ctg atc cag tgacaatgtg cccctgccca 436

Gly Cys Pro Ala Val Ala Leu Ile Gln

125

gccggggctc gccactcat cattcattca tccattctag agccagtctc tgcctcccag 496

acgcggcggg agccaagctc ctccaaccac aaggggggtg gggggcggtg aatcacctcc 556

gaggcctggg tccagggttc aggggaacct tccaaggtgt ctggttgccc tgcctctggc 616

tccagaacag aaaggagcc tcacgctggc tcacacaaaa cagctgacac tgactaagga 676

actgcagcat ttgcacaggg gaggggggtg ccctccttcc tagaggccct gggggccagg 736

ctgacttggg gggcagactt gacactaggc cccactcact cagatgtcct gaaattccac 796

cacgggggtc accctggggg gttagggacc tatttttaac actagggggc tggcccacta 856

ggagggtg ccctaagata cagaccccc caactcccca aagcggggag gagatattta 916

ttttggggag agtttggagg ggaggagaa ttattaata aaagaatctt taacttt 973

<210> 178

<211> 129

<212> PRT

<213> Homo sapiens

<400> 178

Met Ala Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly

1

5

10

15

Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly

20

25

30

Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys

35

40

45

Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys

50

55

60

Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro  
 65 70 75 80

Ile Leu Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser  
 85 90 95

Gly Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr  
 100 105 110

Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile  
 115 120 125

Gln

<210> 179

<211> 3631

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (191).. (3244)

<400> 179

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ggcgctggcg caagatgatg ttgctccata ttttaaaacg gagccaggcc taccacagat 120

ccacctggaa gggaaccgcc ttgttctcac ctgccttgcc gaaggagct ggcctttgga 180

gttcaagtgg atg cgc gat gac agt gag ctc acc acc tac agc agc gaa 229

Met Arg Asp Asp Ser Glu Leu Thr Thr Tyr Ser Ser Glu

1

5

10

tat aag tac att att cca tct ttg cag aag ctc gat gct ggg ttt tac 277

Tyr Lys Tyr Ile Ile Pro Ser Leu Gln Lys Leu Asp Ala Gly Phe Tyr

15

20

25

cgc tgc gtg gtg cga aac aga atg gga gca ctc ctg caa aga aaa tca 325

Arg Cys Val Val Arg Asn Arg Met Gly Ala Leu Leu Gln Arg Lys Ser

30

35

40

45

gaa gtt caa gtc gca tat atg gga agt ttc atg gat acg gac cag agg 373

Glu Val Gln Val Ala Tyr Met Gly Ser Phe Met Asp Thr Asp Gln Arg

50

55

60

aaa aca gtt tct caa gga cgt gca gcg att cta aac ctg ctg ccc atc 421

Lys Thr Val Ser Gln Gly Arg Ala Ala Ile Leu Asn Leu Leu Pro Ile

65

70

75

acc agc tac ccc aga cct caa gtg act tgg ttt aga gaa ggg cac aag 469

Thr Ser Tyr Pro Arg Pro Gln Val Thr Trp Phe Arg Glu Gly His Lys

80

85

90

att att cca agc aac aga ata gcc atc aca ttg gag aat cag ctg gtg 517

Ile Ile Pro Ser Asn Arg Ile Ala Ile Thr Leu Glu Asn Gln Leu Val  
95 100 105

atc ctc gcc acc aca acc agt gat gcc ggg gca tac tac gtg cag gcc 565  
Ile Leu Ala Thr Thr Thr Ser Asp Ala Gly Ala Tyr Tyr Val Gln Ala  
110 115 120 125

gtg aat gag aaa aat gga gaa aac aag aca agc cca ttc att cat ttg 613  
Val Asn Glu Lys Asn Gly Glu Asn Lys Thr Ser Pro Phe Ile His Leu  
130 135 140

agc ata gca aga gat gtt ggc aca cct gaa acc atg gcc cca acc att 661  
Ser Ile Ala Arg Asp Val Gly Thr Pro Glu Thr Met Ala Pro Thr Ile  
145 150 155

gtg gtt ccc ccg ggc aac aga agt gtg gtg gct gga tcc agt gag acc 709  
Val Val Pro Pro Gly Asn Arg Ser Val Val Ala Gly Ser Ser Glu Thr  
160 165 170

acc ttg gaa tgt ata gcc agt gcc agg cct gtg gag gac ctg agt gtg 757  
Thr Leu Glu Cys Ile Ala Ser Ala Arg Pro Val Glu Asp Leu Ser Val  
175 180 185

acc tgg aag agg aat gga gtg aga atc acc agt ggc ctc cac agc ttt 805  
Thr Trp Lys Arg Asn Gly Val Arg Ile Thr Ser Gly Leu His Ser Phe  
190 195 200 205

gga aga cgc ctc acc atc agc aac ccg acg tcc gcg gac acc ggg cca 853  
Gly Arg Arg Leu Thr Ile Ser Asn Pro Thr Ser Ala Asp Thr Gly Pro



tac ctg gat gta acc aat atc gct cca gtg ttc acc cag cgg cca gtg 1237

Tyr Leu Asp Val Thr Asn Ile Ala Pro Val Phe Thr Gln Arg Pro Val

335

340

345

gac acc aca gtt act gac ggg atg aca gcc att cta agg tgt gag gtg 1285

Asp Thr Thr Val Thr Asp Gly Met Thr Ala Ile Leu Arg Cys Glu Val

350

355

360

365

tcc ggg gct ccc aaa ccc gcc atc acc tgg aaa aga gaa aac cac att 1333

Ser Gly Ala Pro Lys Pro Ala Ile Thr Trp Lys Arg Glu Asn His Ile

370

375

380

ctg gcc agt ggc tct gtc cgg att cct agg ttc atg ctt ctt gaa tcg 1381

Leu Ala Ser Gly Ser Val Arg Ile Pro Arg Phe Met Leu Leu Glu Ser

385

390

395

ggg ggt cta cag atc gcg ccc gtc ttc atc cag gat gcc ggc aac tac 1429

Gly Gly Leu Gln Ile Ala Pro Val Phe Ile Gln Asp Ala Gly Asn Tyr

400

405

410

acc tgc tat gcg gcc aac aca gag ggc tcc ctg aat gca tcg gcc acg 1477

Thr Cys Tyr Ala Ala Asn Thr Glu Gly Ser Leu Asn Ala Ser Ala Thr

415

420

425

ctc act gtg tgg aat cgg acg tcc atc gtc cac cct cct gag gac cac 1525

Leu Thr Val Trp Asn Arg Thr Ser Ile Val His Pro Pro Glu Asp His

430

435

440

445

gtg gtg att aag ggg acc acg gcc acg ctg cac tgt ggt gcc aca cat 1573  
 Val Val Ile Lys Gly Thr Thr Ala Thr Leu His Cys Gly Ala Thr His  
 450 455 460

gac ccc cgg gtt tca ctc cgc tac gtt tgg aag aag gac aac gtg gcc 1621  
 Asp Pro Arg Val Ser Leu Arg Tyr Val Trp Lys Lys Asp Asn Val Ala  
 465 470 475

ctg act cca tcg agc acg tct agg atc gtg gtg gag aag gac ggg tcc 1669  
 Leu Thr Pro Ser Ser Thr Ser Arg Ile Val Val Glu Lys Asp Gly Ser  
 480 485 490

ctt ctc atc agc cag acg tgg tca ggc gac atc ggt gac tac agc tgc 1717  
 Leu Leu Ile Ser Gln Thr Trp Ser Gly Asp Ile Gly Asp Tyr Ser Cys  
 495 500 505

gag att gtt tct gaa gga ggg aat gac tcc agg atg gcc cgg ctg gaa 1765  
 Glu Ile Val Ser Glu Gly Gly Asn Asp Ser Arg Met Ala Arg Leu Glu  
 510 515 520 525

gtg att gaa ctg cct cat tca cct cag aac ctc ctg gtc agc cct aat 1813  
 Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn  
 530 535 540

tct tcc cac agc cac gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat 1861  
 Ser Ser His Ser His Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp  
 545 550 555

gga aac agt cct att ctt tat tac atc gtg gag ctg tct gaa aac aac 1909  
 722/735



Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn  
560 565 570

tct cca tgg aag gtg cat ctg tca aac gtt ggc cct gag atg aca ggc 1957  
Ser Pro Trp Lys Val His Leu Ser Asn Val Gly Pro Glu Met Thr Gly  
575 580 585

gtc acc gtg agt ggc ctg act ccg gct cgt acc tat caa ttc cgg gtg 2005  
Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val  
590 595 600 605

tgc gcg gtg aat gaa gtg ggc agg ggc cag tac agt gcc gag aca agc 2053  
Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser  
610 615 620

agg ttg atg cta cct gaa gaa cca ccc agt gct ccc ccg aaa aat ata 2101  
Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile  
625 630 635

gtg gcc agt ggg cgg act aat cag tcc att atg gtc cag tgg cag cca 2149  
Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro  
640 645 650

ccc cca gaa aca gag cac aac ggg gtg ttg cgt gga tac atc ctc agg 2197  
Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg  
655 660 665

tac cgc ctg gct ggc ctt ccc gga gag tac cag cag cgg aac atc acc 2245  
Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr  
723/735

670 675 680 685

agc ccg gag gtg aac tac tgc ctg gtg aca gac ctg atc atc tgg aca 2293  
Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr

690 695 700

cag tat gag ata cag gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc 2341  
Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val

705 710 715

ttc agc agg gca gtg acc gag tac acc ttg cag gga gtg ccc acc gcg 2389  
Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala

720 725 730

ccc ccg cag aac gtg cag acg gaa gcc gtg aac tcc acc acc att cag 2437  
Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln

735 740 745

ttc ctg tgg aac cct ccg cct cag cag ttt atc aat ggc atc aac cag 2485  
Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln

750 755 760 765

gga tac aag ctt ctg gca tgg ccg gca gat gcc ccc gag gct gtc act 2533  
Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr

770 775 780

gtg gtc act att gcc cca gat ttc cac gga gtc cac cat gga cac ata 2581  
Val Val Thr Ile Ala Pro Asp Phe His Gly Val His His Gly His Ile

785 790 795

724/735

acg aac ctg aag aag ttt acc gcc tac ttc act tcc gtt ctg tgc ttc 2629  
Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe  
800 805 810

acc acc cct ggg gac ggg cct ccc agc aca cct cag ctg gtc tgg act 2677  
Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr  
815 820 825

cag gaa gac aaa cca gga gct gtg gga cat ctg agt ttc aca gag atc 2725  
Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile  
830 835 840 845

ttg gac aca tct ctc aag gtc agc tgg cag gag ccc ctg gag aaa aat 2773  
Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn  
850 855 860

ggc atc att act ggc tat cag atc tct tgg gaa gtg tac ggc agg aac 2821  
Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn  
865 870 875

gac tct cgt ctc acg cac acc ctg aac agc acg acg cac gag tac aag 2869  
Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr Thr His Glu Tyr Lys  
880 885 890

atc caa ggc ctc tca tct ctc acc acc tac acc atc gac gtg gcc gct 2917  
Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala  
895 900 905



tcttcctttg aattttttat attcttttctt tctctttttt gtttcttctt ctttgagtat 3374

tttgtaatct tactgggagg gctaaagcgt cttctatcat atcgaattgg gacaatgata 3434

gaagacaatc ttgtttttgt cactctaaag aaattattgt aagattttat catcaggtat 3494

gacatttaca ccattgatgt aggccttttta aaaaatatat ccagcctgta ttgggttaag 3554

atgattcttt tctgatcctg atttcttagg agttgggtttt ttttttttta aagcataaat 3614

aaattttaatt gcatcag 3631

- <210> 180
- <211> 1018
- <212> PRT
- <213> Homo sapiens

<400> 180

Met Arg Asp Asp Ser Glu Leu Thr Thr Tyr Ser Ser Glu Tyr Lys Tyr  
1 5 10 15

Ile Ile Pro Ser Leu Gln Lys Leu Asp Ala Gly Phe Tyr Arg Cys Val  
20 25 30

Val Arg Asn Arg Met Gly Ala Leu Leu Gln Arg Lys Ser Glu Val Gln  
35 40 45

Val Ala Tyr Met Gly Ser Phe Met Asp Thr Asp Gln Arg Lys Thr Val

50

55

60

Ser Gln Gly Arg Ala Ala Ile Leu Asn Leu Leu Pro Ile Thr Ser Tyr

65

70

75

80

Pro Arg Pro Gln Val Thr Trp Phe Arg Glu Gly His Lys Ile Ile Pro

85

90

95

Ser Asn Arg Ile Ala Ile Thr Leu Glu Asn Gln Leu Val Ile Leu Ala

100

105

110

Thr Thr Thr Ser Asp Ala Gly Ala Tyr Tyr Val Gln Ala Val Asn Glu

115

120

125

Lys Asn Gly Glu Asn Lys Thr Ser Pro Phe Ile His Leu Ser Ile Ala

130

135

140

Arg Asp Val Gly Thr Pro Glu Thr Met Ala Pro Thr Ile Val Val Pro

145

150

155

160

Pro Gly Asn Arg Ser Val Val Ala Gly Ser Ser Glu Thr Thr Leu Glu

165

170

175

Cys Ile Ala Ser Ala Arg Pro Val Glu Asp Leu Ser Val Thr Trp Lys

180

185

190

Arg Asn Gly Val Arg Ile Thr Ser Gly Leu His Ser Phe Gly Arg Arg

195

200

205



365

380

400

415

430

445

460

480

495

510



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820

825

830

Lys Pro Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr

835

840

845

Ser Leu Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile

850

855

860

Thr Gly Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg

865

870

875

880

Leu Thr His Thr Leu Asn Ser Thr Thr His Glu Tyr Lys Ile Gln Gly

885

890

895

Leu Ser Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala

900

905

910

Val Gly Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro

915

920

925

Pro Asp Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser

930

935

940

Pro Arg Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr

945

950

955

960

Ser Ile Ser Arg Trp Ile Val Glu Gly Gln Met Arg His Gln Gly Val

965

970

975

Gly Leu Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu

980

985

990

Pro Ala Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys

995

1000

1005

Tyr Ser Gln Lys Leu Trp Glu Phe Ser Cys

1010

1015

<210> 181

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 181

cttctgctct aaaagctgcg

20

<210> 182

<211> 20

<212> DNA

<213> Artificial Sequence

